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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:37:16 ; Search time 38.333 Seconds

(without alignments)
122.745 Million cell updates/sec

Title: US-10-040-128-1

Perfect score: 86

Sequence: 1 DEINQMHTDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

1291235

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	15	US-10-040-128-1	Sequence 1, Appli
2	78	90.7	15	US-10-040-128-2	Sequence 2, Appli
3	73	84.9	15	US-10-040-128-3	Sequence 3, Appli
4	73	84.9	108	US-10-006-863-6	Sequence 6, Appli
5	73	84.9	108	US-10-395-032-6	Sequence 6, Appli
6	73	84.9	784	US-09-905-983-52	Sequence 52, Appli
7	73	84.9	784	US-10-211-462-105	Sequence 105, Appli
8	73	84.9	784	US-10-021-660-99	Sequence 99, Appli
9	73	84.9	784	US-10-174-677-23	Sequence 23, Appli
10	46	53.5	95	US-10-424-599-281094	Sequence 281094, Appli
11	46	53.5	183	US-09-923-298-530	Sequence 530, App
12	46	53.5	183	US-10-102-806-550	Sequence 530, App
13	46	53.5	192	US-10-188-186-28	Sequence 28, Appli
14	46	53.5	193	US-09-764-853-673	Sequence 673, App
15	45	52.3	418	US-10-282-122A-74566	Sequence 74566, A

16	45	52.3	1312	US-10-369-493-1904	Sequence 1904, Ap
17	44	51.2	88	US-10-424-599-186878	Sequence 186878,
18	44	51.2	165	US-10-424-599-177622	Sequence 177622,
19	44	51.2	387	US-10-424-599-233597	Sequence 233597,
20	44	51.2	443	US-10-425-114-39166	Sequence 39166, A
21	44	51.2	558	US-10-369-493-6392	Sequence 6392, Ap
22	44	51.2	731	US-10-424-599-172399	Sequence 172399,
23	43	50.0	105	US-09-864-408A-6804	Sequence 6804, Ap
24	43	50.0	367	US-10-282-122A-51530	Sequence 51530, A
25	42	48.8	166	US-10-437-963-142823	Sequence 142823,
26	42	48.8	230	US-10-437-963-104838	Sequence 104838,
27	42	48.8	254	US-09-864-761-33770	Sequence 33770, A
28	42	48.8	261	US-10-424-599-283374	Sequence 283374,
29	42	48.8	515	US-10-424-599-166030	Sequence 166030,
30	42	48.8	1039	US-09-900-237-14	Sequence 14, Appli
31	42	48.8	1103	US-10-408-765A-2255	Sequence 2255, Ap
32	41	47.7	122	US-10-424-599-187689	Sequence 187689,
33	41	47.7	167	US-10-243-552-596	Sequence 596, App
34	41	47.7	294	US-10-424-599-153982	Sequence 153982,
35	41	47.7	494	US-10-369-493-20846	Sequence 20846, A
36	41	47.7	549	US-10-424-599-186879	Sequence 186879,
37	41	47.7	551	US-10-424-599-186880	Sequence 186880,
38	41	47.7	587	US-10-424-599-235268	Sequence 235268,
39	41	47.7	657	US-10-276-774-1900	Sequence 1900, Ap
40	41	47.7	712	US-09-978-295A-264	Sequence 264, App
41	41	47.7	722	US-09-978-697-264	Sequence 264, App
42	41	47.7	722	US-09-978-192A-264	Sequence 264, App
43	41	47.7	722	US-09-999-832A-264	Sequence 264, App
44	41	47.7	722	US-09-978-189-264	Sequence 264, App
45	41	47.7	772	US-09-978-608A-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-10-040-128-1
; Sequence 1, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang
; APPLICANT: Hicklin, Daniel J.
; APPLICANT: Bohlen, Peter
; TITLE OF INVENTION: Antibody Antagonists of VE-Cadherin Without Adverse Effects on
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-1

Query Match 100.0%; Score 86; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEINQMHTDEKNE 15
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Db 1 DEINQMHTDEKNE 15

RESULT 2
US-10-040-128-2
; Sequence 2, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang

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; APPLICANT: Hicklin, Daniel J.
; TITLE OF INVENTION: Antibody Antagonists of Vb-Cadherin without Adverse Effects on
; FILE REFERENCE: 11245/46976
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-040-128-2

Query Match
Best Local Similarity 90.7%; Score 78; DB 13; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 15
Db 1 DWIMQMHIIDEKN 15

RESULT 3
US-10-040-128-3
; Sequence 3, Application US/10040128
; Publication No. US2002016003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang
; APPLICANT: Hicklin, Daniel J.
; TITLE OF INVENTION: Antibody Antagonists of Vb-Cadherin without Adverse Effects on
; FILE REFERENCE: 11245/46976
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-040-128-3

Query Match
Best Local Similarity 84.9%; Score 73; DB 13; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
Db 1 DWIMQMHIIDEKN 14

RESULT 4
US-10-006-869-6
; Sequence 6, Application US/10006869
; Publication No. US2003008216A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
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; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-006-869-6

Query Match
Best Local Similarity 84.9%; Score 73; DB 14; Length 108;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
Db 5 DWIMQMHIIDEKN 18

RESULT 5
US-10-395-032-6
; Sequence 6, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-395-032-6

Query Match
Best Local Similarity 84.9%; Score 73; DB 15; Length 108;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
Db 5 DWIMQMHIIDEKN 18

RESULT 6
US-09-905-983-52
; Sequence 52, Application US/09905983
; Patent No. US20020045591A1
; GENERAL INFORMATION:
; APPLICANT: Geiger, Benjamin
; APPLICANT: Ben-Ze'ev, Avri
; APPLICANT: Sadot, Eilat
; TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
; FILE REFERENCE: 01/22326
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 52
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-983-52

Query Match
Best Local Similarity 84.9%; Score 73; DB 9; Length 784;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
Db 48 DWIMQMHIIDEKN 61
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RESULT 7
US-10-211-462-105
; Sequence 105, Application US/10211462
; Publication No. US2004003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasia
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 105
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-105

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Query Match      84.9%; Score 73; DB 12; Length 784;
Best Local Similarity 92.9%; Pred. No. 0.0072;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 DEINQMHIDEKN 14
Db      48 DWINQMHIDEKN 61

```

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RESULT 8
US-10-021-660-99
; Sequence 99, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-99

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Query Match      84.9%; Score 73; DB 14; Length 784;
Best Local Similarity 92.9%; Pred. No. 0.0072;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 DEINQMHIDEKN 14

```

```

Db      48 DWINQMHIDEKN 61

RESULT 9
US-10-174-677-23
; Sequence 23, Application US/10174677
; Publication No. US2003019070A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Ting
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANCHORING STEM CELLS IN A MICROENVIRONMENT
; FILE REFERENCE: 40716(1P-012)
; CURRENT APPLICATION NUMBER: US/10/174,677
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-677-23

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Query Match      84.9%; Score 73; DB 14; Length 784;
Best Local Similarity 92.9%; Pred. No. 0.0072;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 DEINQMHIDEKN 14
Db      48 DWINQMHIDEKN 61

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RESULT 10
US-10-424-599-281094
; Sequence 281094, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 281094
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9584C.1.pap
US-10-424-599-281094

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Query Match      53.5%; Score 46; DB 12; Length 95;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY      1 DEINQMHIDEKN 12
Db      18 DQNNHMHDOQ 29

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RESULT 11
US-09-925-298-530
; Sequence 530, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; PRIOR FILING DATE: 2001-08-10

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; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 530
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (81)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-530

Query Match      53.5%; Score 46; DB 12; Length 183;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY      1 DEINWQHIDEKNE 15
Db      122 EEVWDKLMMDKEKE 136

RESULT 12
US-10-102-806-530
; Sequence 530; Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 530
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (81)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-530

Query Match      53.5%; Score 46; DB 14; Length 183;
Best Local Similarity 40.0%; Pred. No. 25;
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Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY      1 DEINWQHIDEKNE 15
Db      122 EEVWDKLMMDKEKE 136

RESULT 13
US-10-188-186-28
; Sequence 28; Application US/10188186
; Publication No. US20040029789A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-397C
; CURRENT APPLICATION NUMBER: US/10/188,186
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/360814
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/303828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/323380
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/361133
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/304016
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/373881
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/305673
; PRIOR FILING DATE: 2001-07-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: Custom
; SEQ ID NO 28
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-186-28

Query Match      53.5%; Score 46; DB 12; Length 192;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY      1 DEINWQHIDEKNE 15
Db      131 EEVWDKLMMDKEKE 145

RESULT 14
US-09-764-853-673
; Sequence 673; Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 673
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-673

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Query Match      53.5%; Score 46; DB 9; Length 193;
Best Local Similarity 40.0%; Pred. No. 26;
Matches      6; Conservative      7; Mismatches      2; Indels      0; Gaps      0;

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Qy      1 DEINOMHIDEKNE 15
Db      132 EEVMDKIMDKERKE 146

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RESULT 15
US-10-282-122A-74566
; Sequence 74566, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamanoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 74566
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74566

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Query Match      52.3%; Score 45; DB 12; Length 418;
Best Local Similarity 42.9%; Pred. No. 85;
Matches      6; Conservative      5; Mismatches      3; Indels      0; Gaps      0;

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```

Qy      2 EIWNOHIDEKNE 15
Db      14 EIWDAIHAEEERKE 27

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Search completed: July 29, 2004, 11:50:32
Job time : 38.3333 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:32:25 ; Search time 13 Seconds

(without alignments)
59,568 Million cell updates/sec

Title: US-10-040-128-1

Sequence: 1 DEINQMHIIDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/ECTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	84.9	108	4	US-09-187-859-6 Sequence 6, Appli
2	73	84.9	108	4	US-09-839-542B-6 Sequence 6, Appli
3	73	84.9	108	4	US-09-535-852-6 Sequence 6, Appli
4	73	84.9	780	1	US-08-188-228-50 Sequence 50, Appli
5	73	84.9	780	1	US-08-332-643-44 Sequence 44, Appli
6	73	84.9	780	1	US-08-332-638-50 Sequence 50, Appli
7	40	46.5	747	4	US-09-134-000C-6641 Sequence 6641, Ap
8	40	46.5	1114	4	US-09-637-145-4 Sequence 8, Appli
9	40	46.5	1122	4	US-10-072-094-8 Sequence 4, Appli
10	40	46.5	1122	4	US-10-072-094-91 Sequence 8, Appli
11	39.5	45.9	138	4	US-09-570-921-5 Sequence 91, Appli
12	39.5	45.9	128	3	US-08-965-036-87 Sequence 87, Appli
13	39.5	45.9	613	3	US-09-257-490-14 Sequence 14, Appli
14	39.5	45.3	148	4	US-09-621-976-4783 Sequence 4783, Ap
15	39	45.3	226	4	US-09-533-029-88 Sequence 88, Appli
16	39	45.3	231	4	US-09-345-473E-16 Sequence 36, Appli
17	39	45.3	535	2	US-08-933-750C-20 Sequence 20, Appli
18	39	45.3	535	3	US-09-234-613-20 Sequence 20, Appli
19	39	45.3	535	3	US-09-023-942A-10 Sequence 10, Appli
20	38.5	44.8	138	4	US-09-570-921-6 Sequence 85, Appli
21	38.5	44.8	198	3	US-08-965-056-85 Sequence 5, Appli
22	38.5	44.8	417	1	US-08-118-469A-5 Sequence 13, Appli
23	38.5	44.8	417	1	US-08-909-119-5 Sequence 13, Appli
24	38	44.2	110	4	US-09-187-859-13 Sequence 13, Appli
25	38	44.2	110	4	US-09-839-542B-13 Sequence 13, Appli
26	38	44.2	110	4	US-09-535-852-13 Sequence 121, App
27	38	44.2	135	4	US-09-732-210-121

28	38	44.2	163	4	US-10-072-094-4 Sequence 4, Appli
29	38	44.2	326	4	US-09-345-473E-10 Sequence 10, Appli
30	38	44.2	532	1	US-08-188-228-44 Sequence 44, Appli
31	38	44.2	532	1	US-08-332-638-44 Sequence 44, Appli
32	38	44.2	653	3	US-09-107-532A-4502 Sequence 4502, Ap
33	38	44.2	734	4	US-09-134-000C-5602 Sequence 5602, Ap
34	38	44.2	780	4	US-10-072-094-93 Sequence 93, Appli
35	38	44.2	793	1	US-08-188-228-54 Sequence 54, Appli
36	38	44.2	793	1	US-08-332-643-48 Sequence 48, Appli
37	38	44.2	793	1	US-08-332-638-54 Sequence 54, Appli
38	38	44.2	799	1	US-08-188-228-42 Sequence 42, Appli
39	38	44.2	799	1	US-08-332-638-42 Sequence 42, Appli
40	38	44.2	800	4	US-09-555-790A-2 Sequence 2, Appli
41	38	44.2	855	4	US-10-072-094-9 Sequence 9, Appli
42	38	44.2	879	4	US-10-072-094-90 Sequence 2, Appli
43	38	44.2	938	4	US-09-637-145-2 Sequence 90, Appli
44	38	44.2	1011	4	US-09-637-145-2 Sequence 89, Appli
45	38	44.2	1069	4	US-10-072-094-87 Sequence 87, Appli

ALIGNMENTS

RESULT 1
US-09-187-859-6
; Sequence 6, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-859-6

Query Match 84.9%; Score 73; DB 4; Length 108;
Best Local Similarity 92.9%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKKN 14
Db 5 DWINQMHIIDEKKN 18

RESULT 2
US-09-839-542B-6
; Sequence 6, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-6

Query Match 84.9%; Score 73; DB 4; Length 108;
Best Local Similarity 92.9%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
| | | | | | | | | | | | | | | |
Db 5 DWIMQMHIIDEKN 18

RESULT 3
US-09-535-852-6

Sequence 6, Application US/09535852

Patent No. 6638911

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James M.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

FILE REFERENCE: 100086.407C6

CURRENT APPLICATION NUMBER: US/09/535,852

CURRENT FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 2009

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 108

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-535-852-6

Query Match 84.9%; Score 73; DB 4; Length 108;
Best Local Similarity 92.9%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
| | | | | | | | | | | | | | | |
Db 5 DWIMQMHIIDEKN 18

RESULT 4
US-08-188-228-50

Sequence 50, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,460

FILING DATE: 19 APR 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5597725and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 780 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-188-228-50

Query Match 84.9%; Score 73; DB 1; Length 780;
Best Local Similarity 92.9%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
| | | | | | | | | | | | | | | |
Db 44 DWIMQMHIIDEKN 57

RESULT 5
US-08-332-643-44

Sequence 44, Application US/08332643

Patent No. 5639634

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray &

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/872,643

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5639634and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 780 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-643-44

Query Match 84.9%; Score 73; DB 1; Length 780;
Best Local Similarity 92.9%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
| | | | | | | | | | | | | | | |

Db 44 DWINOMHIDEKN 57

RESULT 6

US-08-332-638-50
Sequence 50, Application US/08332638
Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shinaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: BorunSTREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: ChicagoSTATE: Illinois
COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 780 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-638-50

Query Match 84.9%; Score 73; DB 1; Length 780;

Best Local Similarity 92.9%; Pred. No. 0.0022;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINOMHIDEKN 14

Db 44 DWINOMHIDEKN 57

RESULT 7

US-09-134-000C-6641

Sequence 6641, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patent in version 3.1

SEQ ID NO 6641
LENGTH: 747
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6641

Query Match

Best Local Similarity 46.5%; Score 40; DB 4; Length 747;

Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 EIVNOMHIDEKN 14

Db 705 EIVNOMHIDEKN 717

RESULT 8

US-09-637-145-4

Sequence 4, Application US/09637145

Patent No. 6673587

GENERAL INFORMATION:

APPLICANT: EVANS, RONALD M.

APPLICANT: KAO, HUNG-YING

APPLICANT: DOMNES, MICHAEL

APPLICANT: ORDENTLICH, PETER

TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR

FILE REFERENCE: SALK3000

CURRENT APPLICATION NUMBER: US/09/637,145

CURRENT FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 4

LENGTH: 1114

TYPE: PRT

ORGANISM: Mus sp.

US-09-637-145-4

Query Match 46.5%; Score 40; DB 4; Length 1114;

Best Local Similarity 62.5%; Pred. No. 4.1e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINOMH 8

Db 781 DTWNEMH 788

RESULT 9

US-10-072-094-8

Sequence 8, Application US/10072094

Patent No. 6600351

GENERAL INFORMATION:

APPLICANT: JACKSON, DONALD

APPLICANT: LORENZI, MATTHEW

APPLICANT: ATTAR, RICARDO

APPLICANT: GOTTARDIS, MARCO

TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES

FILE REFERENCE: 3053-4145US1

CURRENT APPLICATION NUMBER: US/10/072,094

CURRENT FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 60/298,296

PRIOR FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 127

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 8

LENGTH: 1122

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-094-8

Query Match 46.5%; Score 40; DB 4; Length 1122;

Best Local Similarity 62.5%; Pred. No. 4.2e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINOMH 8

Db 789 DTWNEMH 796

RESULT 10
US-10-072-094-91
Sequence 91, Application US/10072094

Patent No. 6600351
GENERAL INFORMATION:
APPLICANT: JACKSON, DONALD
APPLICANT: LORENZI, MATTHEW
APPLICANT: ATTAR, RICARDO
APPLICANT: GOTTARDIS, MARCO
TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
FILE REFERENCE: 3053-4145US1
CURRENT APPLICATION NUMBER: US/10/072,094
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/238,296
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 91
LENGTH: 1122
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-094-91

Query Match Similarity 46.5%; Score 40; DB 4; Length 1122;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQM 8
Db 789 DTWNEMH 796

RESULT 11
US-09-570-921-5
Sequence 5, Application US/09570921

Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERIES: PIERRE-FRANCOIS
APPLICANT: LORENZI, MATTHEW
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 5
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-5

Query Match Similarity 45.9%; Score 39.5; DB 4; Length 138;
Best Local Similarity 26.3%; Pred. No. 51;
Matches 10; Conservative 2; Mismatches 3; Indels 23; Gaps 1;

QY 1 DEINQM-----HIDEXNE 15
Db 81 DDINMTWQWKEISNYTGIIYLIIESQIQEKNE 118

RESULT 12
US-08-965-056-87
Sequence 87, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovastnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-87

Query Match Similarity 45.9%; Score 39.5; DB 3; Length 198;
Best Local Similarity 26.3%; Pred. No. 75;
Matches 10; Conservative 2; Mismatches 3; Indels 23; Gaps 1;

QY 1 DEINQM-----HIDEXNE 15
Db 150 DDINMTWQWKEISNYTGIIYLIIESQIQEKNE 187

RESULT 13
US-09-257-490-14

Sequence 14, Application US/09257490A
Patent No. 6248328
GENERAL INFORMATION:
APPLICANT: Dietrich, Ursula
APPLICANT: Von Briesen, Hagen
APPLICANT: Grez, Manuel
APPLICANT: Rubsamem-Waigmann, Helga
TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its differential
TITLE OF INVENTION: diagnostics, a vaccine against HIV-1 virus infections
TITLE OF INVENTION: of this subtype and method of producing same, use of
FILE REFERENCE: 10496/PS8512US1
CURRENT APPLICATION NUMBER: US/09/257,490A
CURRENT FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 14
LENGTH: 613
TYPE: PRT
ORGANISM: Human immunodeficiency virus
FEATURE:
OTHER INFORMATION: HIV-1 (Mal)
US-09-257-490-14

Query Match 45.9%; Score 39.5; DB 3; Length 613;
 Best Local Similarity 25.3%; Pred. No. 2.6e+02;
 Matches 10; Conservative 2; Mismatches 3; Indels 23; Gaps 1;

QY 1 DEIMNQMH-----HIDEKNE 15
 Db 514 DDIMNNMTMMQWKEKISNYGTGIYNIRESQIQEKNE 551

RESULT 14
 US-09-621-976-4783
 ; Sequence 4783, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621.976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 4783
 ; LENGTH: 148
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-621-976-4783

Query Match 45.3%; Score 39; DB 4; Length 148;
 Best Local Similarity 41.7%; Pred. No. 65;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNOQHIDEKNE 15
 Db 97 WOIHHTEDKDK 108

RESULT 15
 US-09-533-029-88
 ; Sequence 88, Application US/09533029
 ; Patent No. 6664446
 ; GENERAL INFORMATION:
 ; APPLICANT: Heard, Jacqueline
 ; APPLICANT: Broun, Pierre
 ; APPLICANT: Riechmann, Jose-Luis
 ; APPLICANT: Keddie, James
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Adam, Luc
 ; APPLICANT: Samaha, Raymond
 ; APPLICANT: Zhang, James
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Pilgrim, Marsha
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Reuber, Lynne
 ; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
 ; FILE REFERENCE: MFI-010
 ; CURRENT APPLICATION NUMBER: US/09/533.029
 ; CURRENT FILING DATE: 2000-03-22
 ; EARLIER APPLICATION NUMBER: 60/125,814
 ; EARLIER FILING DATE: 1999-03-23
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 88
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: G221
 US-09-533-029-88

Query Match 45.3%; Score 39; DB 4; Length 226;
 Best Local Similarity 55.6%; Pred. No. 1e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEIMNQMH 9
 Db 214 DDIMSSMHL 222

Search completed: July 29, 2004, 11:38:39
 Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:30:55 ; Search time 31 Seconds

(without alignments)
152.670 Million cell updates/sec

Title: US-10-040-128-1

Sequence: 1 DEIMNQMHIDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phase:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	73	84.9	782	6 Q8WNW5	Q8WNW5 sus scrofa
2	50	58.1	77	16 Q8Y643	Q8Y643 listeria mo
3	50	58.1	773	13 Q8AYD0	Q8AYD0 gallus gall
4	49	57.0	77	16 Q92AF1	Q92AF1 listeria in
5	47	54.7	712	5 Q20323	Q20323 caenorhabdi
6	46	53.5	241	11 Q9D996	Q9D996 mus musculu
7	46	53.5	520	8 Q8B916	Q8B916 pleistodont
8	46	53.5	933	4 Q8N768	Q8N768 homo sapien
9	46	53.5	1029	4 Q9C099	Q9C099 homo sapien
10	46	53.5	9341	5 Q813N9	Q813N9 plasmodium
11	45	52.3	176	10 Q8RYF1	Q8RYF1 arena strig
12	45	52.3	264	16 Q8YJ65	Q8YJ65 bradyrhizob
13	45	52.3	391	16 Q31773	Q31773 bacillus su
14	45	52.3	502	5 Q61644	Q61644 caenorhabdi
15	45	52.3	787	16 Q8F093	Q8F093 leptospira
16	45	52.3	847	11 Q9CDE1	Q9CDE1 mus musculu

17	45	52.3	942	16 Q87S90	Q87S90 vibrrio para
18	45	52.3	993	11 Q9DC06	Q9DC06 mus musculu
19	45	52.3	1682	4 Q15054	Q15054 homo sapien
20	45	52.3	2273	3 Q42823	Q42823 saccharomyc
21	44	51.2	558	5 Q20375	Q20375 caenorhabdi
22	44	51.2	566	5 Q95277	Q95277 caenorhabdi
23	43.5	50.6	1422	5 Q81380	Q81380 plasmodium
24	43	50.0	92	10 Q8LSF0	Q8LSF0 gossypium h
25	43	50.0	171	10 Q04666	Q04666 arabidopsis
26	43	50.0	243	6 Q7Y8P8	Q7Y8P8 sus scrofa
27	43	50.0	367	16 Q97KM0	Q97KM0 clostridium
28	43	50.0	425	16 Q7V243	Q7V243 prochloroco
29	43	50.0	444	16 Q93XC5	Q93XC5 staphylococ
30	43	50.0	487	16 Q83HS6	Q83HS6 tropheryma
31	43	50.0	487	16 Q83G54	Q83G54 tropheryma
32	43	50.0	712	5 Q81IC7	Q81IC7 plasmodium
33	43	50.0	876	15 Q9QSS4	Q9QSS4 human immun
34	43	50.0	900	10 Q9FM50	Q9FM50 arabidopsis
35	43	50.0	1710	5 Q81239	Q81239 plasmodium
36	43	50.0	2285	5 Q81240	Q81240 plasmodium
37	42.5	49.4	844	15 Q41789	Q41789 human immun
38	42.5	49.4	845	15 Q9GRB1	Q9GRB1 human immun
39	42.5	49.4	866	15 Q73296	Q73296 human immun
40	42	48.8	157	5 Q9NFS8	Q9NFS8 plasmodium
41	42	48.8	157	17 Q8PZJ1	Q8PZJ1 methanosarc
42	42	48.8	166	16 Q98F49	Q98F49 rhizobium l
43	42	48.8	237	16 Q7VFM5	Q7VFM5 helicobacte
44	42	48.8	296	16 Q7Y8R5	Q7Y8R5 synechococ
45	42	48.8	342	11 Q8C915	Q8C915 mus musculu

ALIGNMENTS

RESULT 1
Q8WNW5 PRELIMINARY; PRT; 782 AA.
AC Q8WNW5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VB cadherin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirano M., Hirano K., Nishimura J., Kanaide H.;
RT "Transcriptional up-regulation of p27Kip1 during contact-induced
RT growth arrest in the endothelial cells.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99119339; PubMed=9918666;
RA Hirano M., Nitro N., Hirano K., Nishimura J., Harshorne D.J.,
RA Kanaide H.;
RT "Expression, subcellular localization and cloning of the 130 kDa
RT regulatory subunit of myosin phosphatase in porcine aortic endothelial
RL cells.";
RL Biochem. Biophys. Res. Commun. 254:490-496(1999).
CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
CC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
CC SORTING OF HETEROGENEOUS CELL TYPES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AB046120; BAB82983.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.


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Db          62 DELWEAYLDEKXK 76

RESULT 5
Q20323      PRELIMINARY;      PRT;      712 AA.
AC Q20323;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN F42C5.4.
OS Caenorhabditis elegans.
OC Rhabditiidae; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC NCB1_TaxID=6239;
OX NCB1_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RT "The sequence of C. elegans cosmid F42C5.";
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U40799; AAA81480.1; -.
DR PIR; T16338; T16338.
DR WormPep; F42C5.4; CE04557.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Hypothetical protein.
SQ SEQUENCE 712 AA; 84368 MW; 06A97B962739F6 CRC64;

Query Match          54.7%; Score 47; DB 5; Length 712;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY          1 DEINWOMH 8
DB          341 DEINWOMH 348

RESULT 6
Q9D996      PRELIMINARY;      PRT;      241 AA.
AC Q9D996;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1700122011Rik.
GN 1700122011Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H. H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
RA Blake J., Boffelli D., Bojunga N., Carinini P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
RA Hayaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007241; BAB24910.1; -.
DR MGD; MGI:1923901; 1700122011Rik.
SQ SEQUENCE 241 AA; 27288 MW; D2A47C328823597E CRC64;

Query Match          53.5%; Score 46; DB 11; Length 241;
Best Local Similarity 40.0%; Pred. No. 18;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY          1 DEINWOMHIDEKNE 15
DB          38 EDINWIKIEEBEE 52

RESULT 7
Q9B916      PRELIMINARY;      PRT;      520 AA.
AC Q9B916;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cytochrome oxidase subunit I (RC 1.9.3.1) (COI) (Cytochrome c oxidase
DE polypeptide I) (Fragment).
OS Pleistodontes rigisamos.
OG Pleistodontes.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC Agonidae; Agoninae; Pleistodontes.
OX NCB1_TaxID=108973;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=GW943;
RX Weiblen G.D.;
RT "Phylogenetic analyses of dioecious fig pollinators based on
RT mitochondrial DNA sequences and morphology.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
CC C + 2 H(2)O.
CC -1- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF200409; AAK00121.1; -.
DR HSSP; P18401; 1FFT.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.

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DR GO: GO:0009481; F:a3-lyse cytochrome c oxidase; IEA.
 DR GO: GO:0009482; F:a3-lyse cytochrome c oxidase; IEA.
 DR GO: GO:0009483; F:ca3-lyse cytochrome c oxidase; IEA.
 DR GO: GO:0009484; F:cb3-lyse cytochrome c oxidase; IEA.
 DR GO: GO:0009485; F:cb3-lyse cytochrome c oxidase; IEA.
 DR GO: GO:0016429; F:cytochrome-c oxidase activity; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR GO: GO:0006110; P:transport; IEA.
 DR InterPro: IPR00883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 DR Copper; Electron transport; Heme; Inner membrane; Membrane;
 KM Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KM Mitochondrion.
 FT NON TER
 SQ SEQUENCE 520 AA; 58939 MW; 315025C557C5A7F1 CRC64;

Query Match 53.5%; Score 46; DB 8; Length 520;
 Best Local Similarity 52.9%; Pred. No. 41;
 Matches 9; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 DEINWQMHIDEKNE 15
 :|||:|:|:|:
 Db 492 EIMWNSPIYIDEVND 508

RESULT 8
 Q8N768 PRELIMINARY; PRT; 933 AA.
 ID Q8N768
 AC Q8N768;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Hypothetical protein KIAA1764.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RA Strausberg R.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC030701; AAH30701.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003885; LRR_cyst.
 DR InterPro: IPR007092; LRR_SDS22.
 DR Pfam: PF00560; LRR; 4.
 DR SMART: SM00365; LRR_SD22; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 933 AA; 108165 MW; 66831C7105DAB3C CRC64;

Query Match 53.5%; Score 46; DB 4; Length 933;
 Best Local Similarity 46.7%; Pred. No. 76;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DEINWQMHIDEKNE 15
 :|||:|:|:|:
 Db 62 DHINWQHLDLSNQ 76

RESULT 9
 Q9C099 PRELIMINARY; PRT; 1029 AA.
 ID Q9C099
 AC Q9C099;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Hypothetical protein KIAA1764 (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 DE MEDLINE=21082932; PubMed=11214970;
 RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XIX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 7:347-351(2000).
 DR EMBL: AB051551; BAB21855.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003603; LRRcap.
 DR InterPro: IPR007092; LRR_SDS22.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00560; LRR; 4.
 DR SMART: SM00446; LRRcap; 1.
 KM Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 1029 AA; 119884 MW; 1817DD4D446462DB CRC64;

Query Match 53.5%; Score 46; DB 4; Length 1029;
 Best Local Similarity 46.7%; Pred. No. 85;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DEINWQMHIDEKNE 15
 :|||:|:|:|:
 Db 59 DHINWQHLDLSNQ 73

RESULT 10
 Q8I3N9 PRELIMINARY; PRT; 9341 AA.
 ID Q8I3N9
 AC Q8I3N9;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PFE1120W.
 OS Plasmodium falciparum (isolate 3D7).
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=36329;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
 RA Hall N., Bowman S., Churcher C., Quail M., Barrett B.;
 RL Submitted (Sep-2002) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22255708; PubMed=12368867;
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
 RA Humphray S., Jagels K., James K.D., Johnson D., Kexhrou A.,
 RA Knights A., Konfortov B., McLean J., Mooney P., Moule S., Murphy L.,
 RA line A., Maddison M., Kyles S., Larke N., Lawson D., Leonard N.,
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitch E.,
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders S., Stevens M.,
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
 RA Sulston J.E., Craig A., Newbold C., Barrett B.G.;
 RT "Sequence of plasmodium falciparum chromosomes 1, 3-9 and 13."
 RL Nature 419:527-531(2002).
 DR EMBL: AL929353; CAD51588.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 9341 AA; 1121395 MW; BAE88CDEDF66B92D CRC64;

Query Match 53.5%; Score 46; DB 5; Length 9341;
 Best Local Similarity 42.9%; Pred. No. 8.6e+02;

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DEINQWIDEKN 14
 6064 NDIMNDIHINKTN 6077

RESULT 11
 Q8RYFL PRELIMINARY; PRT; 176 AA.
 AC Q8RYFL
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative resistance protein (Fragment).
 GN RGA.
 OS *Avena strigosa* (black oat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Avenae; Avena.
 OC NCBI_TaxID=38783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lorce Y., Irtigoyen M.L., Fominaya A., Ferrer E.,
 RT "Resistance gene analogous in *Avena strigosa*."
 RL Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ437574; CAD26862.1; -
 DR GO; GO:0005524; P-ATP binding; IEA.
 DR GO; GO:0006915; P-apoptosis; IEA.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00931; NB-ARC; 1.
 FT NON_TER 1 176
 FT NON_TER 1 176
 SQ SEQUENCE 176 AA; 20133 MW; D60982A15C6FE2F6 CRC64;

Query Match 52.3%; Score 45; DB 10; Length 176;
 Best Local Similarity 58.3%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 INQWIDEKN 14
 62 LKMSNIDEKD 73
 Db
 RESULT 12
 Q89JB9 PRELIMINARY; PRT; 264 AA.
 AC Q89JB9
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE BL15364 protein.
 GN BL15364
 OS *Bradyrhizobium japonicum*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OC NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2248498; PubMed=12597275;
 RA Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idegawa K., Irtiguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsunooka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005954; BAC50629.1; -
 DR GO; GO:0005874; C-microtubule; IEA.
 DR GO; GO:0005198; F-structural molecule activity; IEA.
 DR GO; GO:0007018; P-microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta_tubulin.

DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
 QW Complete proteome.
 SQ SEQUENCE 264 AA; 28370 MW; DFF6604CED986052 CRC64;

Query Match 52.3%; Score 45; DB 16; Length 264;
 Best Local Similarity 42.9%; Pred. No. 30;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DEINQWIDEKN 14
 212 DQYMAAHVDEDMN 225

RESULT 13
 Q31773 PRELIMINARY; PRT; 391 AA.
 AC Q31773
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Penicillin-binding protein.
 GN PPBX.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berteiro M.G., Bessieres P., Bolojin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignani S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conneron I.F., Cumange N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Erttington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz S.Y., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallier N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Iraya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,
 RA Prescan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S.,
 RA Sorokin M., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpeira P., Tognoni K.,
 RA Toesto V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,
 RA Viati A., Wandut R., Wedler B., Wedler H., Weltzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoko K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 subtilis".
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.,
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99112; CAB13568.1; -
 DR PIR; C69673; C69673.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR Complete proteome.
 SQ SEQUENCE 391 AA; 43858 MW; 08D3D7AB99826CE CRC64;

Query Match 52.3%; Score 45; DB 16; Length 391;

Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EIMNQHIDEKNE 15
|||:|:|:|
36 IWNALHRSENE 48

Db 36 IWNALHRSENE 48

RESULT 14

061644 PRELIMINARY; PRT; 502 AA.

AC 061644; DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DE Putative PP2C protein phosphatase FEM-2.

OS Caenorhabditis briggsae.

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6238;

RP SEQUENCE FROM N.A.

RC STRAIN=AF16;

RT "Molecular Evolution of a Sex Determination Protein: FEM-2 (PP2C) in

Caenorhabditis."

CC EMBL: AF054982; AAC08602.1; -

DR GO: GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO: GO:0016787; F:hydrolase activity; IEA.

DR GO: GO:0000287; F:magnesium ion binding; IEA.

DR GO: GO:0004722; F:protein serine/threonine phosphatase activity; IEA.

DR InterPro: IPR000222; PP2C.

DR InterPro: IPR001932; PP2C-like.

DR Pfam: PF00481; PP2C.1.

DR SMART: SM00332; PP2C.1.

DR SMART: SM00331; PP2C-STG.1.

DR PROSITE: PS01032; PP2C.1.

DR Hydrolase; Magnesium.

DR SEQUENCE 502 AA; 57327 MW; 9EC5F1F8FF799A41 CRC64;

QY 2 EIMNQHIDEKNE 15
::|||:|:|:|
481 DLRMWKIDESDE 494

Db 481 DLRMWKIDESDE 494

QY 2 EIMNQHIDEKNE 15

Db 481 DLRMWKIDESDE 494

QY 2 EIMNQHIDEKNE 15

Db 481 DLRMWKIDESDE 494

QY 2 EIMNQHIDEKNE 15

Db 481 DLRMWKIDESDE 494

DR InterPro: IPR000917; Sulfatase.

DR Pfam: PF00884; Sulfatase; 1.

KW Complete proteome.

DR SEQUENCE 787 AA; 91636 MW; 1BF953631B28F798 CRC64;

QY 2 EIMNQHIDEKNE 14
|||:|:|:|
176 EIMNQHIDEKNE 188

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

QY 2 EIMNQHIDEKNE 14

Db 176 EIMNQHIDEKNE 188

Search completed: July 29, 2004, 11:37:08
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:30:30 ; Search time 6.66667 Seconds

(without alignments)
117.158 Million cell updates/sec

Title: US-10-040-128-1
Perfect score: 86
Sequence: 1 DEIMNQMHIDEKNE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	90.7	784	1 CAD5_MOUSE	P55284 mus musculu
2	73	84.9	784	1 CAD5_PIG	O02840 sus scrofa
3	73	84.9	784	1 CAD5_HUMAN	P31351 homo sapien
4	45	52.3	418	1 GLYA_STRP3	O84788 streptococc
5	45	52.3	418	1 GLYA_STRP8	O84722 streptococc
6	45	52.3	418	1 GLYA_STRP1	O99321 streptococc
7	45	52.3	418	1 GLYA_STRP1	O99321 streptococc
8	43	50.0	435	1 HPA1_YEAST	P57201 buchnera ap
9	42	48.8	363	1 DPX3_BUCAP	O84983 buchnera ap
10	42	48.8	363	1 DPX3_BUCAP	O84983 buchnera ap
11	41	47.7	772	1 CAD7_HUMAN	O94111 homo sapien
12	41	47.7	772	1 CAD7_HUMAN	O94111 homo sapien
13	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
14	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
15	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
16	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
17	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
18	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
19	40	46.5	271	1 AROE_CLOPE	P82136 hoplosternu
20	39.5	45.9	859	1 ENY_FV1MA	P04583 human immun
21	39.5	45.9	859	1 ENY_FV1MA	P04583 human immun
22	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
23	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
24	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
25	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
26	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
27	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
28	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
29	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
30	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
31	39	45.3	146	1 HBB_BRATR	O36021 schizosacch
32	38.5	44.8	863	1 ENY_FV1Z8	P05882 human immun
33	38	44.2	135	1 R9J_PYRAB	O94195 pyrococcus

ALIGNMENTS

RESULT 1	ID	CAD5_MOUSE	STANDARD;	PRT;	784 AA.
AC	P55284; O35542;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Vascular endothelial-cadherin precursor (VE-cadherin) (CDH5).				
GN	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain capillary;				
RX	MEDLINE=96141083; PubMed=8555485;				
RA	Breier G., Breviario F., Cavada L., Berthier R., Schnuerch H.,				
RA	Gotsch U., Westweder D., Risau W., Dejana E.;				
RT	"Molecular cloning and expression of murine vascular endothelial-				
RT	cadherin in early stage development of cardiovascular system.";				
RL	Blood 87:630-641(1996).				
RN	[2]				
RP	REVIEWS TO 67-70.				
RA	Breviario F.;				
RL	Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A., AND FUNCTION.				
RC	STRAIN=BA1B/c; TISSUE=Breast carcinoma;				
RX	MEDLINE=97364256; PubMed=9220534;				
RA	Matsuyoshi N., Imamura S.;				
RT	"In vivo evidence of the critical role of cadherin-5 in murine				
RT	vascular integrity.";				
RT	Proc. Assoc. Am. Physicians 109:362-371(1997).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6; TISSUE=Brain;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diachenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,				
RA	Rah S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Boesk S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,				
RA	Schmerch A., Schein J.E., Jones S.J.M., Maira M.A.;				

34	38	44.2	135	1	RS9_PYRPU	O80427 pyrococcus
35	38	44.2	135	1	RS9_PYRPU	O59299 pyrococcus
36	38	44.2	146	1	HBE_HYLSY	O95190 hylobates s
37	38	44.2	254	1	FTSQ_HAEIN	P45067 haemophilus
38	38	44.2	276	1	KDUI_BACHD	O94400 bacillus ha
39	38	44.2	311	1	Y467_MYCCE	O48650 mycoplasma
40	38	44.2	315	1	SPDE_NICSY	O48650 mycoplasma
41	38	44.2	315	1	SPDI_HYONI	O48650 mycoplasma
42	38	44.2	317	1	SPDI_HYONI	O48650 mycoplasma
43	38	44.2	342	1	SPDE_LYCES	O96557 datura stra
44	38	44.2	420	1	GLYA_STRMU	O92455 lycopersico
45	38	44.2	427	1	CISY_SALTY	O8467 streptococc
						O68883 salmonella

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X83930; CAAS8782.2; -;
 CC EMBL; D63942; BAA2617.1; -;
 CC EMBL; BC054790; AAH54790.1; -;
 CC HSSP; P15116; INCI.
 CC MGD; MGI:105057; Cdh5.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C_term.
 CC Pfam; PF00028; cadherin_5.
 CC Pfam; PF01049; Cadherin_C_term; 1.
 CC PRINTS; PR00205; CADHERIN_C.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT PROPEP 1 24 POTENTIAL.
 FT CHAIN 25 45 POTENTIAL.
 FT TRANSMEM 46 784 VASCULAR ENDOTHELIAL-CADHERIN.
 FT TRANSMEM 46 593 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 594 620 POTENTIAL.
 FT DOMAIN 621 784 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 46 149 CADHERIN 1.
 FT DOMAIN 150 256 CADHERIN 2.
 FT DOMAIN 257 371 CADHERIN 3.
 FT DOMAIN 372 476 CADHERIN 4.
 FT DOMAIN 477 593 CADHERIN 5.
 FT DOMAIN 738 753 SER-RICH.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 784 AA; 87902 MW; 7B75698DE2F7E160 CRC64;
 Query Match 90.7%; Score 78; DB 1; Length 784;
 Best Local Similarity 93.3%; Pred. No. 5; 9e-05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DEINQMHIIDEKN 15
 DB 46 DWINQMHIIDEKN 60
 RESULT 2
 CAD5_PIG STANDARD; PRT; 782 AA.
 AC 002840;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5).
 GN Cdh5.
 OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kilshaw P.J.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions. It
 CC associates with alpha-catenin forming a link to the cytoskeleton
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Found at cell-cell
 CC boundaries and probably at cell-matrix boundaries (by similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y13919; CAA74225.1; -;
 CC HSSP; P09803; IEDH.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C_term.
 CC Pfam; PF00028; cadherin_5.
 CC Pfam; PF01049; Cadherin_C_term; 1.
 CC PRINTS; PR00205; CADHERIN_C.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT PROPEP 1 22 POTENTIAL.
 FT CHAIN 23 44 VASCULAR ENDOTHELIAL-CADHERIN.
 FT TRANSMEM 45 592 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 593 619 POTENTIAL.
 FT DOMAIN 620 782 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 149 255 CADHERIN 1.
 FT DOMAIN 256 370 CADHERIN 2.
 FT DOMAIN 371 475 CADHERIN 3.
 FT DOMAIN 476 592 CADHERIN 4.
 FT DOMAIN 736 751 CADHERIN 5.
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 782 AA; 87546 MW; 7403F974E2DF782F CRC64;
 Query Match 84.9%; Score 73; DB 1; Length 782;
 Best Local Similarity 92.9%; Pred. No. 0.00038;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DEINQMHIIDEKN 14
 DB 45 DWINQMHIIDEKN 58
 RESULT 3
 CAD5_HUMAN STANDARD; PRT; 784 AA.
 AC P3151;
 DT 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5)
 DB (7B4 antigen) (CD144 antigen).
 GN CDH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endothelial cells;
 RX MEDLINE=95353875; PubMed=7627717;
 RA Breviaro F., Cavada L., Corada M., Martin-Padura I., Navarro P.,
 RA Golay J., Introna M., Gulino D., Lampugnani M.G., Dejana E.,
 RT "Functional properties of human vascular endothelial cadherin
 RT (7B4/cadherin-5), an endothelium-specific cadherin,"
 RL Arterioscler. Thromb. Biol. 15:1229-1239(1995).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97362755; PubMed=9219219;
 RA Ali U., Liao F., Martens E., Muller W.A.;
 RT "Vascular endothelial cadherin (VE-cadherin): cloning and role in
 RT endothelial cell-cell adhesion,"
 RL Microcirculation 4:267-277(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shintoyama Y., Tsujimoto G., Kitajima M., Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins,"
 RL Biochem. J. 349:159-167(2000).
 RN [4]
 RP SEQUENCE OF 5-784 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins
 RT in nervous tissue,"
 RL Cell Regul. 2:261-270(1991).
 RN [5]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Endothelial cells;
 RX MEDLINE=92394977; PubMed=1522121;
 RA Lampugnani M.G., Resnati M., Raiteri M., Pigott R., Pisacane A.,
 RA Hohen G., Ruco L.P., Dejana E.;
 RT "A novel endothelial-specific membrane protein is a marker of
 RT cell-cell contacts,"
 RL J. Cell Biol. 118:1511-1522(1992).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions. It
 CC associates with alpha-catenin forming a link to the cytoskeleton.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Found at cell-cell
 CC boundaries and probably at cell-matrix boundaries.
 CC -1- TISSUE SPECIFICITY: Endothelial tissues and brain.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -1- DATABASE: NAME=PROV. NOTE=CD guide CD144 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd144.htm".
 CC
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DR EMBL; X79981; CAA56306.1; -
 DR EMBL; U84722; AAB41796.1; -
 DR EMBL; AB035304; BAA87418.1; -
 DR EMBL; X59796; CAA42468.1; -
 DR PIR; S49893; ITHUCS.
 DR HSSP; P15116; INCU.
 DR GlycoStidB; P33151; -
 DR Genew; HGNC:1764; CDH5.
 DR MIM; 601120; -
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5-term.
 DR Pfam; PF01049; cadherin_C_term; 1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL. 1 25
 FT PROPEP. 26 47
 FT CHAIN. 48 784
 FT DOMAIN. 48 593
 FT TRANSMEM. 594 620
 FT DOMAIN. 621 784
 FT DOMAIN. 48 151
 FT DOMAIN. 152 258
 FT DOMAIN. 259 372
 FT DOMAIN. 373 477
 FT DOMAIN. 478 593
 FT DOMAIN. 736 753
 FT CARBOHYD. 61 61
 FT CARBOHYD. 112 112
 FT CARBOHYD. 157 157
 FT CARBOHYD. 362 362
 FT CARBOHYD. 442 442
 FT CARBOHYD. 523 523
 FT CARBOHYD. 535 535
 FT CONFLICT. 517 517
 SQ SEQUENCE 784 AA; 87516 MW; F643BFC222A599DE CRC64;
 T -> I (IN REF. 2 AND 4).
 Query Match 84.9%; Score 73; DB 1; Length 784;
 Best Local Similarity 92.9%; Pred. No. 0.00038;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DEINQMHIDEKN 14
 Db 48 DWIWMHIDEKN 61
 ID GLYA_STRP3 STANDARD; PRT; 418 AA.
 AC Q8K7H8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
 DE (SMT).
 GN GLYA OR SPYM3 0803 OR SPS1002.
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=198466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206;
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff U.S.,
 RA Mammarella N.D., Liu W.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,

RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RA "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 RX STRAIN=SSI-1 / Serotype M3;
 RX MEDLINE=22683278; PubMed=12799345;
 RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayashi H., Hattori M., Hamada S.;
 RA "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 RT large-scale genomic rearrangement in invasive strains and new insights
 RT into phage evolution";
 RT Genome Res. 13:1042-1055(2003).
 CC -1- FUNCTION: Interconversion of serine and glycine.
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine +
 CC H(2)O = tetrahydrofolate + L-serine.
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Key enzyme in the biosynthesis of purines, lipids,
 CC hormones and other components.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the SHMT family.
 CC -----
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 CC -----
 DR EMBL; AE014152; AAM79410.1; -.
 DR EMBL; AP005144; BAC64097.1; ALT_INIT.
 DR HAMAP; MF_00051; -. 1
 DR InterPro; IPR001085; Gly_HyMettransf.
 DR Pfam; PF00464; SHMT; 1.
 DR PROSITE; PS00096; SHMT; 1.
 KW Transferase; Pyridoxal phosphate; One-carbon metabolism;
 FT Complete proteome.
 FT BINDING 230 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT SEQUENCE 418 AA; 45079 MW; 1C3D5E167C13650 CRC64;
 SQ
 Query Match 52.3%; Score 45; DB 1; Length 418;
 Best Local Similarity 42.9%; Pred. No. 7;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EIMNOMHIDEKNE 15
 Db 14 EIMDAIHAEERQE 27
 ID GLYA_STRP8 STANDARD; PRT; 418 AA.
 AC Q8P122;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
 DE (SHMT).
 GN GLYA OR SPYM18.1105.
 OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=186103;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108;

RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RA "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RX STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RL
 CC -1- FUNCTION: Interconversion of serine and glycine.
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine +
 CC H(2)O = tetrahydrofolate + L-serine.
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Key enzyme in the biosynthesis of purines, lipids,
 CC hormones and other components.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the SHMT family.
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 CC -----
 DR EMBL; AE010036; AAL97727.1; -.
 DR HAMAP; MF_00051; -. 1
 DR InterPro; IPR001085; Gly_HyMettransf.
 DR Pfam; PF00464; SHMT; 1.
 DR PROSITE; PS00096; SHMT; 1.
 KW Transferase; Pyridoxal phosphate; One-carbon metabolism;
 FT Complete proteome.
 FT BINDING 230 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT SEQUENCE 418 AA; 45065 MW; ASE8A48CD419CASA CRC64;
 SQ
 Query Match 52.3%; Score 45; DB 1; Length 418;
 Best Local Similarity 42.9%; Pred. No. 7;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EIMNOMHIDEKNE 15
 Db 14 EIMDAIHAEERQE 27
 ID GLYA_STRPY STANDARD; PRT; 418 AA.
 AC Q992P1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
 DE (SHMT).
 GN GLYA OR SPY1145.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RL
 CC -1- FUNCTION: Interconversion of serine and glycine.
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine +
 CC H(2)O = tetrahydrofolate + L-serine.
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Key enzyme in the biosynthesis of purines, lipids,
 CC hormones and other components.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the SHMT family.

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CC -1- PATHWAY: Key enzyme in the biosynthesis of purines, lipids,
CC hormones and other components.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the SHMT family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE006556; AAK34017.1; -.
CC HSSP; P00477; IDPO.
CC DR HAMAP; MF_00051; -.
CC DR InterPro; IPR001085; Gly_HyMettransf.
CC DR Pfam; PF00464; SHMT; 1.
CC DR PROSITE; PS00096; SHMT; 1.
CC DR Transferase; Pyridoxal phosphate; One-carbon metabolism;
CC KW Complete proteome.
CC FT BINDING 230 230 PYRIDOXAL PHOSPHATE (By similarity).
CC SQ SEQUENCE 418 AA; 45096 MW; AF475E79D41D9A1F CRC64;
CC -----
CC Query Match 52.3%; Score 45; DB 1; Length 418;
CC Best Local Similarity 42.9%; Pred. No. 7;
CC Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
CC -----
CC QY 2 DEIMNQHIDEKNE 15
CC |:::|:::|
CC Db 14 ELMDAIHAEERQE 27
CC -----
CC RESULT 7
CC ID HPA1_YEAST STANDARD; PRT; 2273 AA.
CC AC P32874;
CC DT 01-OCT-1993 (Rel. 27, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE HPA1 protein.
CC GN HPA1 OR YMR207C OR YMR261.01C OR YMR325.08C.
CC OS Saccharomyces cerevisiae (Baker's Yeast).
CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CC OX NCBI_TaxID=4932;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=S288C / AB972;
CC RX MEDLINE=97313268; PubMed=9169872;
CC RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
CC Connor R., Dedman K., Devlin K., Gencles S., Hamlin N., Hunt S.,
CC Jagers K., Lye G., Moutle S., Odell C., Pearson D., Rajandream M.A.,
CC Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;
CC RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
CC XIII".
CC RL Nature 387:90-93(1997).
CC [2]
CC RP SEQUENCE OF 125-949 FROM N.A.
CC RX MEDLINE=9416412; PubMed=7906156;
CC RA Kearsey S.E.;
CC RT "Identification of a Saccharomyces cerevisiae gene closely related to
CC RT FAS3 (acetyl-CoA carboxylase)".
CC RL DNA Seq. 4:69-70(1993).
CC -1- COFACTOR: Biotin (By similarity).
CC -1- SIMILARITY: STRONG, TO ACETYL-COA CARBOXYLASE.
CC -1- CAUTION: The reading frame from which this protein in translated
CC has no Met initiation codon near to the 5' end. It does not seem to
CC be a pseudogene. There are no apparent frameshifts.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z49809; CAA89922.1; -.
CC DR EMBL; Z48755; CAA88647.1; -.
CC DR EMBL; Z22558; CAA80280.1; -.
CC DR PIR; S55089; S55089.
CC DR HSSP; P24182; IDV1.
CC DR Geronline; 142893; -.
CC DR SGD; S0004820; HPA1.
CC DR InterPro; IPR001882; Biotin BS.
CC DR InterPro; IPR005482; Biotin carb C.
CC DR InterPro; IPR000089; Biotin_lipoyl.
CC DR InterPro; IPR000022; Carboxyl_trans.
CC DR InterPro; IPR005479; Cpase_L_D2.
CC DR InterPro; IPR005481; Cpase_L_N.
CC DR Pfam; PF02785; Biotin carb C; 1.
CC DR Pfam; PF00364; biotin_lipoyl; 1.
CC DR Pfam; PF01039; Carboxyl_trans; 1.
CC DR Pfam; PF00289; Cpase_L_chain; 1.
CC DR Pfam; PF02786; Cpase_L_D2; 1.
CC DR PROSITE; PS00188; BIOTIN; 1.
CC DR PROSITE; PS00866; CPASE_1; 1.
CC DR PROSITE; PS00867; CPASE_2; 1.
CC DR Biotin; Ligase; ATP-binding.
CC FT NP BIND 332 337
CC FT ACT SITE 459 459 ATP (By similarity).
CC FT BINDING 804 804 BIOTIN (By similarity).
CC FT CONFLICT 661 661 F -> L (IN REF. 2).
CC SQ SEQUENCE 2273 AA; 259160 MW; 08727A301549DA92 CRC64;
CC -----
CC Query Match 52.3%; Score 45; DB 1; Length 2273;
CC Best Local Similarity 53.8%; Pred. No. 43;
CC Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 1 DEIMNQHIDEK 13
CC |:::|:::|
CC Db 1248 DEVEQHIDPER 1260
CC -----
CC RESULT 8
CC ID H1SX_BUCAL STANDARD; PRT; 435 AA.
CC AC P57201;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Histidinol dehydrogenase (EC 1.1.1.23) (HHD).
CC GN H1SD OR BU100.
CC OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
CC symbiotic bacterium).
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Buchnera.
CC OX NCBI_TaxID=118099;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Tokyo 1998;
CC RX MEDLINE=20445173; PubMed=10993077;
CC RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
CC RT "Genome sequence of the endocellular bacterial symbiont of aphids
CC RT Buchnera sp. Aps.".
CC RL Nature 407:81-86(2000).
CC -1- FUNCTION: Catalyzes the sequential NAD-dependent oxidations of L-
CC histidinol to L-histidinoldehyde and then to L-histidine (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: L-histidinol + 2 NAD(+) + H2O = L-histidine
CC + 2 NADH.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- PATHWAY: Histidine biosynthesis; ninth (last) step.
CC -1- SUBUNIT: Homodimer (By similarity).

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CC -1- SIMILARITY: Belongs to the histidinol dehydrogenase family.
CC -----
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CC -----
CC EMBL: AB001118; BAB12819.1; -.
CC HAMAP: MF_01024; -.
CC InterPro: IPR001692; Histidinol_dh.
CC Pfam: PF00815; Histidinol_dh.1.
CC PRINTS: PR00083; H0LIDHGRNASE.
CC ProDom: PD002680; H0LIDHGRNASE.
CC TIGRFAMs: TIGR00069; hsd.1.
CC PROSITE: PS00611; HISOL_DEHYDROGENASE; 1.
CC Histidine biosynthesis; Oxidoreductase; NAD; Metal-binding; Zinc;
CC Complete proteome.
CC ACT_SITE 327 327 BY SIMILARITY.
CC FT ACT_SITE 328 328 ZINC (BY SIMILARITY).
CC METAL 260 260 ZINC (BY SIMILARITY).
CC METAL 263 263 ZINC (BY SIMILARITY).
CC METAL 361 361 ZINC (BY SIMILARITY).
CC METAL 420 420 ZINC (BY SIMILARITY).
CC SEQUENCE 435 AA; 47843 MW; 83DD3DC4E43430E CRC64;

Query Match 50.0%; Score 43; DB 1; Length 435;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 WNNQNHIDEK 13
Db 10 WNKLPDEOK 19

RESULT 9
DP3X_BUCAP STANDARD; PRT; 363 AA.
AC Q8K983;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III subunit gamma (EC 2.7.7.7).
GN DNAX OR BUSG46.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
CC NCB1_TaxID=98794;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=22084549; PubMed=12089438;
CC Tamas I., Klason L., Canhaeck B., Naeslund A.K., Eriksson A.-S.,
CC Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
CC "50 million years of genomic strais in endosymbiotic bacteria.";
CC Science 296:2376-2379(2002).
CC -1- FUNCTION: DNA polymerase III is a complex, multichain enzyme
CC responsible for most of the replicative synthesis in bacteria.
CC This DNA polymerase also exhibits 3' to 5' exonuclease activity.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA) (N).
CC -1- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIII complex. PolIII associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex (by similarity).
CC -----
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CC -----
CC EMBL: AB014123; AAM68009.1; -.
CC InterPro: IPR003593; AAA_Atpase.
CC InterPro: IPR003959; AAA_Atpase_cent.
CC InterPro: IPR001270; Chadrinn_cipa/B.
CC InterPro: IPR008921; Pol_clamp_load_C.
CC InterPro: IPR000862; Pfdomain.
CC Pfam: PF00004; AAA.1.
CC PRINTS: PR00300; CLPPEPTASEA.
CC SMART: SM00382; AAA.1.
CC Transferrase; DNA-directed DNA polymerase; DNA replication;
CC ATP-binding; Complete proteome.
CC NP_BIND 45 52 ATP (POTENTIAL).
CC SEQUENCE 363 AA; 42186 MW; F22762B7493B091A CRC64;

Query Match 48.8%; Score 42; DB 1; Length 363;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EWNQNHIDEKNE 15
Db 300 KIMNOLFIKNNENE 313

RESULT 10
PHG1_HUMAN STANDARD; PRT; 1113 AA.
ID PHG1_HUMAN
AC Q9ULI1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pleckstrin homology domain containing family G member 1 (Fragment).
GN PLEKHG1 OR KIAA1203.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCB1_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE=Brain;
CC MEDLINE=20039619; PubMed=10574462;
CC Nagase T., Ishikawa K.-I., Kikuno R., Hiroseawa M., Nomura N.,
CC Ohara O.;
CC "Prediction of the coding sequences of unidentified human genes. XV.
CC The complete sequences of 100 new cDNA clones from brain which code
CC for large proteins in vitro.";
CC DNA Res. 6:337-345(1999).
CC -1- SIMILARITY: Contains 1 PH domain.
CC -----
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CC -----
CC EMBL: AB03035; BAA6523.1; -.
CC Genew; HGNC:20884; PLEKHG1.
CC InterPro: IPR001849; PH.
CC InterPro: IPR000219; RhoGEF.
CC Pfam: PF00169; PH.1.
CC SMART: SM00233; PH.1.
CC PROSITE: PS50003; PH_DOMAIN.1.
CC Hypothetical protein.
CC KW NON TER 1 144 PH.
CC FT DOMAIN 45 144 PH.
CC SEQUENCE 1113 AA; 124624 MW; 62E8E2C698B3519A CRC64;

Query Match 48.8%; Score 42; DB 1; Length 1113;

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Best Local Similarity 53.3%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEIMNQHIDEKKE 15
Db 564 DEIMNDLENYIKKE 578

RESULT 11
CADJ_HUMAN STANDARD; PRT; 772 AA.

AC Q9H159;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cadherin-19 precursor (UNQ478/PRO941).
GN CDH19 OR CDH12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=2045318; PubMed=10995570;
RA Koels P., Van Imschoot G., Van Roy F.;
RT "Characterization of three novel human cadherin genes (CDH7, CDH19, and CDH20) clustered on chromosome 18q22-q23 and with high homology to chicken cadherin-7";
RL Genomics 66:283-295(2000).

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed in many tissues, with the exception of uterus.

CC -1- SIMILARITY: Contains 5 cadherin domains.

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DR EMBL: AJ007607; CAC13126.1; -;
DR EMBL: AY358654; AAG89017.1; -;
DR HSSP: P15116; INCIJ.
DR Genew: HGNC:1758; CDH19.
DR MIM: 603016; -;

DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0007156; P:homophilic cell adhesion; NAS.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00029; cadherin_5.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM0112; CA; 5.

DR PROSITE: PS00232; CADHERIN_1; 2.
DR PROSITE: PS50268; CADHERIN_2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; KW Signal.
FT SIGNAL. 1 21
FT PROPEP 22 43
FT CHAIN 44 772
FT DOMAIN 44 596
FT TRANSMEM 597 617
FT DOMAIN 618 772
FT DOMAIN 44 148
FT DOMAIN 149 256
FT DOMAIN 257 370
FT DOMAIN 371 470

FT DOMAIN 470 581
FT CARBOHYD 57 57
FT CARBOHYD 74 74
FT CARBOHYD 419 419
FT CARBOHYD 437 437
FT CARBOHYD 508 508
FT CARBOHYD 515 515
FT CARBOHYD 516 516
FT CARBOHYD 534 534
SQ SEQUENCE 772 AA; 87002 MW; 650AD27480343C39 CRC64;

Query Match 47.7%; Score 41; DB 1; Length 772;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 INWQHIDEKKN 14
Db 46 INWQFVPEKKN 57

RESULT 12

HBBC_HOPLI STANDARD; PRT; 146 AA.

AC P82316;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin cathectic, beta chain (Hb(Ca) beta chain).
GN HBB.

OS Hoplosternum littorale (Haszari).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Callichthyidae; Hoplosternum.
OX NCBI_TaxID=114109;
RN [1]

RP SEQUENCE, SUBUNIT, AND MASS SPECTROMETRY.

RC TISSUE=Blood;
RX MEDLINE=20298792; PubMed=10747999;
RA Weber R.E., Fago A., Val A.L., Bang A., Van Hauwaert M.-L.,
RT Deswilde S., Zal F., Moens L.;
RT "Isohemoglobin differentiation in the bimodal-breathing amazon catfish Hoplosternum littorale";
RL J. Biol. Chem. 275:17297-17305(2000).

CC -1- FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.

CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.

CC -1- TISSUE SPECIFICITY: Red blood cells.

CC -1- MASS SPECTROMETRY: MW=15978; MW_ERR=0.2; METHOD=Electrospray.

CC The cathodic Hb and anodic Hb display small and large Bohr effects respectively. In addition, the cathodic Hb displays a reverse Bohr effect and appreciable phosphate effects.

CC -1- SIMILARITY: Belongs to the globin family.

DR HSSP: P02142; IOU7.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; Globin_1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 63 63
FT METAL 92 92
SQ SEQUENCE 146 AA; 15976 MW; 4075EB9FC8D3539 CRC64;

Query Match 46.5%; Score 40; DB 1; Length 146;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 INWQHIDE 11
Db 14 INWQHIDE 22

RESULT 13
 AROE CLOPE STANDARD; PRT; 271 AA.
 ID AROE CLOPE STANDARD; PRT; 271 AA.
 AC 08XMT8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Shikimate 5-dehydrogenase (EC 1.1.1.25).
 GN AROE OR CPE0700.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CC NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
 CC NADPH.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC fourth step.
 CC -1- SIMILARITY: Belongs to the shikimate dehydrogenase family.
 CC
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 CC
 CC EMBL: AP003187; BAB80406.1; -
 CC HAMAP: MF_00222; -; 1.
 DR InterPro: IPR006152; Shikimate.
 DR InterPro: IPR006151; Shikimate.DH.
 DR Pfam: PF01488; Shikimate.DH; 1.
 DR TIGRfams: TIGR00507; aroe; 1.
 KW Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
 KM Complete proteome.
 SQ SEQUENCE 271 AA; 30505 MW; 311AF6C6B63ACFE CRC64;

Query Match 46.5%; Score 40; DB 1; Length 271;
 Best Local Similarity 40.0%; Pred. No. 28;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 DEINQMHIDEKNE 15
 Db 247 EIWNGIKVDKSTEE 261

RESULT 14
 PTPA HUMAN STANDARD; PRT; 358 AA.
 ID PTPA HUMAN STANDARD; PRT; 358 AA.
 AC Q15257; Q15258; Q9BXK1; Q9NNZ7; Q9NNZ9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Protein phosphatase 2A, regulatory subunit B' (PP2A, subunit B', PR53
 DE isoform) (phosphotyrosyl phosphatase activator) (PTPA).
 GN PPP2R4 OR PTPA.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM 1).
 RC TISSUE=Heart;
 RX MEDLINE=94253154; PubMed=8195217;

RA Cayla X., Van Hoof C., Bosch M., Waelkens E., Peeters B.,
 RA Merlevede W., Goris J.;
 RT "Molecular cloning, expression, and characterization of PTPA, a
 RT protein that activates the tyrosyl phosphatase activity of protein
 RT phosphatase 2A.";
 RT J. Biol. Chem. 269:15668-15675(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=96015056; PubMed=8530035;
 RA Van Hoof C., Aly M., Garcia A., Cayla X., Cassiman J., Merlevede W.,
 RA Goris J.;
 RT "Structure and chromosomal localization of the human gene of the
 RT phosphotyrosyl phosphatase activator (PTPA) of protein phosphatase
 RT 2A.";
 RL Genomics 28:261-272 (1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
 RX MEDLINE=20341117; PubMed=10880964;
 RA Janssens V., van Hoof C., Martens E., de Baere I., Merlevede W.,
 RA Goris J.;
 RT "Identification and characterization of alternative splice products
 RT encoded by the human phosphotyrosyl phosphatase activator gene.";
 RL Eur. J. Biochem. 267:4406-4413(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hatle J.,
 RA Dictenchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueclin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -1- FUNCTION: Reversibly stimulates the variable phosphotyrosyl
 CC phosphatase activity of PP2A core heterodimer in presence of ATP
 CC and Mg(2+) (in vitro).
 CC -1- SUBUNIT: Associates with PP2A heterodimeric core enzyme, composed
 CC of a 36 kDa catalytic subunit (subunit C) and a 65 kDa constant
 CC regulatory subunit (PR65 or subunit A).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=2; Synonyms=Beta;
 CC IsoId=Q15257-1; Sequence=Displayed;
 CC Name=1; Synonyms=Alpha;
 CC IsoId=Q15257-2; Sequence=VSP_005123;
 CC Name=3; Synonyms=Delta;
 CC IsoId=Q15257-3; Sequence=VSP_005122;
 CC Name=4; Synonyms=Epsilon;
 CC IsoId=Q15257-4; Sequence=VSP_005124;
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC
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CC -----
DR EMBL: X73478; CAA51873.1; -
DR EMBL: X86428; CAA60163.1; -
DR EMBL: X86429; CAA60163.1; JOINED.
DR EMBL: X86430; CAA60163.1; JOINED.
DR EMBL: X86432; CAA60163.1; JOINED.
DR EMBL: X86434; CAA60163.1; JOINED.
DR EMBL: X86435; CAA60163.1; JOINED.
DR EMBL: X86436; CAA60163.1; JOINED.
DR EMBL: X86437; CAA60163.1; JOINED.
DR EMBL: X86438; CAA60163.1; JOINED.
DR EMBL: X86439; CAA60163.1; JOINED.
DR EMBL: X86428; CAB77601.1; -
DR EMBL: X86429; CAB77601.1; JOINED.
DR EMBL: X86430; CAB77601.1; JOINED.
DR EMBL: X86431; CAB77601.1; JOINED.
DR EMBL: X86432; CAB77601.1; JOINED.
DR EMBL: X86433; CAB77601.1; JOINED.
DR EMBL: X86434; CAB77601.1; JOINED.
DR EMBL: X86435; CAB77601.1; JOINED.
DR EMBL: X86436; CAB77601.1; JOINED.
DR EMBL: X86437; CAB77601.1; JOINED.
DR EMBL: X86438; CAB77601.1; JOINED.
DR EMBL: X86439; CAB77601.1; JOINED.
DR EMBL: X86428; CAB77602.1; -
DR EMBL: X86429; CAB77602.1; JOINED.
DR EMBL: X86430; CAB77602.1; JOINED.
DR EMBL: X86431; CAB77602.1; JOINED.
DR EMBL: X86432; CAB77602.1; JOINED.
DR EMBL: X86433; CAB77602.1; JOINED.
DR EMBL: X86434; CAB77602.1; JOINED.
DR EMBL: X86435; CAB77602.1; JOINED.
DR EMBL: X86436; CAB77602.1; JOINED.
DR EMBL: X86437; CAB77602.1; JOINED.
DR EMBL: X86438; CAB77602.1; JOINED.
DR EMBL: X86439; CAB77602.1; JOINED.
DR EMBL: X86428; CAB77603.1; -
DR EMBL: X86429; CAB77603.1; JOINED.
DR EMBL: X86430; CAB77603.1; JOINED.
DR EMBL: X86431; CAB77603.1; JOINED.
DR EMBL: X86432; CAB77603.1; JOINED.
DR EMBL: X86433; CAB77603.1; JOINED.
DR EMBL: X86434; CAB77603.1; JOINED.
DR EMBL: X86435; CAB77603.1; JOINED.
DR EMBL: X86436; CAB77603.1; JOINED.
DR EMBL: X86437; CAB77603.1; JOINED.
DR EMBL: X86438; CAB77603.1; JOINED.
DR EMBL: X86439; CAB77603.1; JOINED.
DR EMBL: BC002545; AAH02545.1; -
DR EMBL: BC011605; AAH11605.1; -
DR PIR: A54021; A54021.
DR Genew: HGNC:9308; PPP2R4.
DR MIM: 600756; -
DR GO: GO:0005625; C:soluble fraction; TAS.
DR GO: GO:0008601; F:protein phosphatase type 2A, intrinsic regn. ; NAS.
DR GO: GO:0008160; F:protein tyrosine phosphatase activator acti. ; TAS.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; NAS.
DR InterPro: IPR004327; Phetyr_phetse_ac.
DR Pfam: PF03095; PRPA; 1.
KW Alternative splicing.
FT VARSPLIC 45 108 Missing (in isoform 3).
FT VARSPLIC 73 107 Missing (in isoform 1).
FT VARSPLIC 73 149 Missing (in isoform 4).
FT VARSPLIC 73 149 Missing (in isoform 4).
FT CONFLICT 113 113 L -> V (IN REF. 4).
FT CONFLICT 297 297 MISSING (IN REF. 2 AND 3).
FT CONFLICT 357 357 S -> V (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 358 AA; 40681 MW; 6A99C21A5F6BB8 CMC64;
Query March 46.5%; Score 40; DB 1; Length 358;
Best Local Similarity 41.7%; Pred. No. 38;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 2 EIMNMHIDEERK 13
Db 72 EWMNEVHEKEQ 83

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RESULT 15
CALX_SCHPO
ID CALX_SCHPO STANDARD; PRT; 560 AA.
AC P365R1;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calnexin homolog precursor.
GN CAL1 OR CNX1 OR SPAC3C7.11C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95347333; PubMed=7621821;
RA Farlati F., Dignard D., Bergeron J.J.M., Thomas D.Y.;
RT "The calnexin homologue cnx1+ in Schizosaccharomyces pombe. is an
RL essential gene which can be complemented by its soluble ER domain.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95181485; PubMed=7876257;
RA Jamatipour M., Rokeach L.A.;
RT "The Schizosaccharomyces pombe homologue of the chaperone calnexin is
RL essential for viability.";
RN [3]
RP J. Biol. Chem. 270:4845-4853 (1995).
RP [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellgett T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkert G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Useery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
CC -!- FUNCTION: Calcium-binding protein that interacts with newly
CC synthesized glycoproteins in the endoplasmic reticulum. It may act
CC in assisting protein assembly and/or in the retention within the
CC ER of unassembled protein subunits. It seems to play a major role
CC in the quality control apparatus of the ER by the retention of
CC incorrectly folded proteins.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
CC reticulum.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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 DR EMBL; M98799; AAA79757.1; -.
 DR EMBL; U13389; AAA58631.1; -.
 DR EMBL; Z93566; CAB16741.1; -.
 DR PIR; S56142; S56142.
 DR GeneDB; Spombe; SPAC3C7.11c; -.
 DR InterPro; IPR009033; Calret_calnex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; Cona_like_lec_g1.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 KM Calcium-binding; Endoplasmic reticulum; Transmembrane; Signal;
 KM Repeat; Chaperone; Glycoprotein.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 560 CALNEXIN HOMOLOG.
 FT DOMAIN 23 489 LUMENAL (POTENTIAL).
 FT TRANSMEM 490 512 POTENTIAL.
 FT DOMAIN 513 560 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 244 310 4 X APPROXIMATE REPEATS.
 FT REPEAT 244 255 1-1.
 FT REPEAT 261 272 1-2.
 FT REPEAT 280 291 1-3.
 FT REPEAT 299 310 1-4.
 FT DOMAIN 314 371 4 X APPROXIMATE REPEATS.
 FT REPEAT 314 324 2-1.
 FT REPEAT 333 343 2-2.
 FT REPEAT 347 357 2-3.
 FT REPEAT 361 371 2-4.
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 560 AA: 63466 MW: E3B2087333E9123 CRC64;

Query Match 46.5%; Score 40; DB 1; Length 560;
 Best Local Similarity 66.7%; Pred. No. 62;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 MHIDEKNE 15
 ||:|||||:
 Db 443 MHVDESNQ 451

Search completed: July 29, 2004, 11:35:22
 Job time : 7.66667 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:31:25 ; Search time 10.333 Seconds

(Without alignments)
139.633 Million cell updates/sec

Title: US-10-040-128-1

Perfect score: 86

Sequence: 1 DEIRNQMTIDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: pirl:
2: pirl:
3: pirl:
4: pirl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	73	84.9	784	1	IJHUC5	cadherin 5 precursor
2	50	58.1	77	2	A11306	hypothetical prote
3	49	57.0	77	2	A11678	hypothetical prote
4	47	54.7	712	2	T16338	hypothetical prote
5	45	52.3	391	2	C69673	penicillin-binding
6	45	52.3	2123	2	S55089	probable acetyl-Co
7	44	51.2	558	2	T29503	serine C-palmitoyl
8	43	50.0	367	2	F97010	fusion, chorismate
9	43	50.0	435	2	C84941	histidinol dehydro
10	43	50.0	444	2	C89768	conserved hypothet
11	42	48.8	524	2	T20872	hypothetical prote
12	42	48.8	549	2	S49446	RING-finger protei
13	41	47.7	201	2	B97339	HAD superfamily hy
14	41	47.7	271	2	A81282	amino acid ABC tra
15	41	47.7	271	2	A81282	amino acid ABC tra
16	41	47.7	380	1	E69541	conserved hypothet
17	41	47.7	467	2	T10854	1-aminocyclopropan
18	41	47.7	519	2	T33616	hypothetical prote
19	41	47.7	532	2	G90607	hypothetical prote
20	41	47.7	2241	2	T20971	hypothetical prote
21	41	47.7	2261	2	T20978	hypothetical prote
22	41	46.5	204	2	T05677	hypothetical prote
23	40	46.5	280	2	F81984	conserved hypothet
24	40	46.5	280	2	H81038	hypothetical prote
25	40	46.5	355	2	T06122	cysteine proteinas
26	40	46.5	455	2	T40940	hypothetical prote
27	40	46.5	459	2	T29945	hypothetical prote
28	40	46.5	460	2	T29946	hypothetical prote
29	40	46.5	560	2	S56142	calcium-binding pr

ALIGNMENTS

RESULT 1
IJHUC5
cadherin 5 precursor - human
N/Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #ext_change 22-Jun-1999
C/Accession: S49893; S24305; A43418
R/Breviario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov
A/Reference number: S49893
A/Accession: S49893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-784 <BRE>
A/Cross-References: EMBL:X79981; NID:G599833; PIDN:CA456306.1; PID:G599834
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: S24305
A/Molecule type: mRNA
A/Residues: 5-516, 'I', 518-784 <SUZ>
A/Cross-References: EMBL:X59796; NID:G639976; PIDN:CA42468.1; PID:G29593
R/Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Houen, G.; Ruco, J.
Cell Biol. 118, 1511-1522, 1992
A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
A/Reference number: A43418; MUID:92394977; PMID:1522121
A/Accession: A43418
A/Molecule type: protein
A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-5
A/Cross-References: EMBL:X59796; NID:G639976; PIDN:CA42468.1; PID:G29593
A/Experimental source: cultured endothelial cells
A/Note: sequence extracted from NCBI database (NCBI:113040, NCBI:113045, NCBI:113047,
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C/Genetics:
A/Gene: GDB:CDH5
A/Cross-References: GDB:134230; OMIM:601120
A/Map position: 16q22.1-16q22.1
C/Supfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane prot
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-47/Domain: propeptide #status predicted <PRO>
F:48-784/Product: cadherin 5 #status predicted <MAT>
F:48-593/Domain: extracellular #status predicted <EXT>
F:50-151/Domain: cadherin repeat homology <CR1>
F:154-258/Domain: cadherin repeat homology <CR2>
F:261-372/Domain: cadherin repeat homology <CR3>
F:375-479/Domain: cadherin repeat homology <CR4>
F:481-587/Domain: cadherin repeat homology <CR5>
F:594-620/Domain: transmembrane #status predicted <TM>
F:621-784/Domain: intracellular #status predicted <INT>
F:736-753/Region: serine-rich

probable acetyl-CoA carboxylase (EC 6.4.1.2) HPA1 - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein YMR261.01c; protein YMR25.08c; protein YMR207c
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 08-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2002
 C/Accession: S55089; S41802; S59447
 R:Dedman, K.; Brown, D.; Bowman, S.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S55089
 A:Accession: S55089
 A:Molecule type: DNA
 A:Residues: 1-833 <DED>
 A:Cross-references: EMBL:Z49809; MIPS:YMR207c; NID:g954459; PIDN:CAA89922.1; PID:g132600
 A:Experimental source: strain AB972
 A>Note: the published sequence extends beyond the amino end
 R:Kearney, S.E.
 submitted to the EMBL Data Library, April 1993
 A:Description: Identification of an *Saccharomyces cerevisiae* gene closely related to PAS
 A:Reference number: S41802
 A:Accession: S41802
 A:Molecule type: DNA
 A:Residues: 1-510, 'U', 512-799 <KEA>
 A:Cross-references: EMBL:Z22558; NID:g296212; PIDN:CAA80280.1; PID:g388250
 A>Note: the published sequence extends beyond the amino end
 R:Odell, C.; Bowman, S.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S59441
 A:Accession: S59447
 A:Molecule type: DNA
 A:Residues: 812-2123 <ODE>
 A:Cross-references: EMBL:Z48755; MIPS:YMR207c; NID:g736296; PIDN:CAA8647.1; PID:g763183
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SGD:HPA1
 A:Cross-references: MIPS:YMR207c; SGD:S0004820
 A:Map position: 13R
 C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
 C:Keywords: biotin binding; ligase
 F:1-487/Domain: biotin carboxylase homology <RCH>
 F:615-687/Domain: lipoyl/biotin-binding homology <LPB>
 F:654/Binding site: biotin (lys) (covalent) #status predicted

Query Match 52.3%; Score 45; DB 2; Length 2123;
 Best Local Similarity 53.8%; Pred. No. 96;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEINQMIDEEK 13
 Db 1098 DEVEQIHPEER 1110

RESULT 7
 T29503
 serie C-palmitoyltransferase (EC 2.3.1.50) F43H9.2 [similarity] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C/Accession: T29503
 R:Mu, X.; Le, T.
 submitted to the EMBL Data Library, February 1996
 A:Description: The sequence of *C. elegans* cosmid F43H9.
 A:Reference number: Z20629
 A:Accession: T29503
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-558 <WUX>
 A:Cross-references: EMBL:U50307; PIDN:AAA92303.1; CESP:F43H9.2
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F43H9.2
 A:Introns: 16/2; 71/3; 115/3; 289/1; 528/3
 C:Superfamily: serine C-palmitoyltransferase chain LCB2; glycine C-acetyltransferase hom
 C:Keywords: acyltransferase; coenzyme A; phosphoprotein; pyridoxal phosphate
 F:18-531/Domain: glycine C-acetyltransferase homology <GGA>
 F:384/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 51.2%; Score 44; DB 2; Length 558;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNMQHIDEEK 15
 Db 29 WNMQHIDDEEE 40

RESULT 8
 F97010
 fusion, chorismate mutase and shikimate 5-dehydrogenase [imported] - *Clostridium acetobu*
 C:Species: *Clostridium acetobutylicum*
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C/Accession: F97010
 R:Mollig, U.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: F97010
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-367 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AK78873.1; PID:g15023795; GSPDB:GN00168
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC0897

Query Match 50.0%; Score 43; DB 2; Length 367;
 Best Local Similarity 63.6%; Pred. No. 28;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEINQMIDEE 11
 Db 341 EIMWIDISIDE 351

RESULT 9
 C84941
 histidinol dehydrogenase (EC 1.1.1.23) [imported] - *Buchnera* sp. (strain APS)
 C:Species: *Buchnera* sp.
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C/Accession: C84941
 R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakai, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000
 A>Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. A
 A:Reference number: A84930; MUID:20445173; PMID:10993077
 A:Accession: C84941
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-435 <STO>
 A:Cross-references: GB:AP000398; GSPDB:GN00144
 A:Experimental source: strain APS
 C:Genetics:
 A:Gene: hsd; BU100
 C:Superfamily: histidinol dehydrogenase; histidinol dehydrogenase homology
 C:Keywords: oxidoreductase

Query Match 50.0%; Score 43; DB 2; Length 435;
 Best Local Similarity 60.0%; Pred. No. 34;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 WNMQHIDEEK 13
 Db 10 WNMQLHPDEOK 19

RESULT 10
 C89768
 conserved hypothetical protein SA0083 [imported] - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: C89768
R/Author: M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C/Species: *Shibub, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirakatsu, K.*
L/Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: C89768
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-444 <KIR>
A/Cross-references: GB:BA000018; PID:G13700003; PIDN:BA41302.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA0083

Query Match 50.0%; Score 43; DB 2; Length 444;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
DB 372 DEWMNGHLDQAVN 385

RESULT 11
T20872
hypothetical protein F26H9.1 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C/Accession: T20872; T21443
R/Sims, M.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19337
A/Accession: T20872
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-524 <WII>
A/Cross-references: EMBL:Z75535; PIDN:CAA99829.1; GSPDB:GN00019; CESP:F26H9.1
A/Experimental source: clone F14B4
R/Baynes, C.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19422
A/Accession: T21443
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-524 <W12>
A/Cross-references: EMBL:Z81516; PIDN:CAB04206.1; GSPDB:GN00019; CESP:F26H9.1
A/Experimental source: clone F26H9
C/Genetics:
A/Gene: CESP:F26H9.1
A/Map position: 1
A/Introns: 49/2; 99/1; 136/1; 186/1; 228/3; 287/3; 346/1; 403/1; 449/3

Query Match 48.8%; Score 42; DB 2; Length 524;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 WNMQHIIDEKN 15
DB 488 WHQRNIDHRNQ 499

RESULT 12
S49446
RING-finger protein - *Lotus japonicus*
C/Species: *Lotus japonicus*
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 23-Mar-2001
C/Accession: S49446
R/Schauser, U.; Borg, S.; Poulsen, C.
submitted to the EMBL Data Library, August 1994
A/Description: Pzf, a gene isolated from a *Lotus japonicus* nodule cDNA library, encodes

A/Reference number: S49445
A/Accession: S49446
A/Molecule type: mRNA
A/Residues: 1-549 <SCH>
A/Cross-references: EMBL:Z6750; NID:G558544; PIDN:CAA6521.1; PID:G558545
A/Experimental source: strain Gifu B-129
C/Superfamily: RING finger homology
C/Keywords: DNA binding; zinc
F/492-543/Domain: RING finger homology <RNG>

Query Match 48.8%; Score 42; DB 2; Length 549;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEINQMHIIDE 11
DB 18 DQNMNMHTDQ 28

RESULT 13
E97339
HAD superfamily hydrolase [imported] - *Clostridium acetobutylicum*
C/Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C/Accession: E97339
R/Nolling, J.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
A/Reference number: A96900; MUID:2135325; PMID:21359325
A/Accession: E97339
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-201 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK81504.1; PID:G15026677; GSPDB:GN00168
A/Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A/Gene: CAC3581

Query Match 47.7%; Score 41; DB 2; Length 201;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EIMNMHIIDE 12
DB 78 EIMNMHIIDE 88

RESULT 14
AB1292
amino acid ABC transporter (binding protein) homolog Imo1738 [imported] - *Listeria monoc.*
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AB1292
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fstli, H.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunet, F.; Kurapat, G.; Madueno, E.; Maitouram, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A./Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AB1292
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-271 <GLA>
A/Cross-references: GB:NC_003210; PIDN:CAC99816.1; PID:G16411192; GSPDB:GN00177
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: Imo1738
C/Superfamily: Lysine-arginine-ornithine-binding protein

Query Match 47.7%; Score 41; DB 2; Length 271;

Best Local Similarity 40.0%; Pred. No. 42;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKNE 15
|:::|:::|:::
Db 198 DEVARYYIDKQKNK 212

RESULT 15

AH1663
amino acid ABC transporter (binding protein) homolog lin1849 [imported] - *Listeria innocua*
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1663
R:Gasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluteler, T.; Simoes, N.; Tixeront, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1663
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-271 <GIA>
A:Cross-references: GB:AL592022; PIDN:CA97080.1; PID:gl6414351; GSPDB:GN00178
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin1849
C:Superfamily: lysine-arginine-ornithine-binding protein

Query Match 47.7%; Score 41; DB 2; Length 271;
Best Local Similarity 40.0%; Pred. No. 42;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 1 DEINQMHIIDEKNE 15
|:::|:::|:::
Db 198 DEVARYYIDKQKNK 212

Search completed: July 29, 2004, 11:37:49
Job time : 11.3333 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:29:40 ; Search time 46.667 Seconds

(without alignments)
90.819 Million cell updates/sec

Title: US-10-040-128-1

Sequence: 1 DEIMWQMHIKKE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Genesepq29Jan04:*
2: genesepq1980s:*
3: genesepq1990s:*
4: genesepq2000s:*
5: genesepq2001s:*
6: genesepq2002s:*
7: genesepq2003s:*
8: genesepq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	15	AAU08777	AAU08777 VE-cadher
2	78	90.7	15	AAU08778	AAU08778 VE-cadher
3	78	90.7	103	AAU08786	AAU08786 Murine VE
4	73	84.9	15	AAU08779	AAU08779 VE-cadher
5	73	84.9	104	AAU08785	AAU08785 Human VE-
6	73	84.9	108	AAV64578	AAV64578 Nonclasti
7	73	84.9	566	AAU11276	AAU11276 Human rec
8	73	84.9	594	AAU11279	AAU11279 Human rec
9	73	84.9	780	AAW25634	AAW25634 Human cad
10	73	84.9	780	AAW13130	AAW13130 Full leng
11	73	84.9	784	ABB81477	ABB81477 Human VE-
12	73	84.9	784	ABU03507	ABU03507 Angiogene
13	73	84.9	784	ABU56570	ABU56570 Lung can
14	73	84.9	784	ADA03363	ADA03363 Human vas
15	50	58.1	77	ABB49545	ABB49545 Listeria
16	46	53.5	183	ABB58822	ABB58822 Breast an
17	46	53.5	192	ADC26203	ADC26203 Human NOV
18	46	53.5	192	ADC10034	ADC10034 Human NOV
19	46	53.5	192	ADC10028	ADC10028 Human NOV
20	46	53.5	193	AAU23017	AAU23017 Novel hum
21	46	53.5	193	ABH10365	ABH10365 Human CDN
22	46	53.5	193	AAU18501	AAU18501 Human end
23	46	53.5	193	ABP66952	ABP66952 Human pol
24	46	53.5	1032	ABR39808	ABR39808 Human SCA
25	45	52.3	418	ABU46642	ABU46642 Protein e

26	45	52.3	420	5	ABP28693	ABP28693 Streptoco
27	43	50.0	105	5	ABP34429	ABP34429 Human red
28	43	50.0	132	4	AAO05753	AAO05753 Human pol
29	43	50.0	367	6	ABU23606	ABU23606 Protein e
30	43	50.0	444	6	ABM73085	ABM73085 Staphyloc
31	42	48.8	75	2	AAV11833	AAV11833 Human 5'
32	42	48.8	145	4	ABG16313	ABG16313 Novel hum
33	42	48.8	254	4	AAU14054	AAU14054 Peptide #
34	42	48.8	254	4	ABH32999	ABH32999 Peptide #
35	42	48.8	254	4	AAW26460	AAW26460 Peptide #
36	42	48.8	254	4	ABR27828	ABR27828 Human pep
37	42	48.8	254	4	ABH18472	ABH18472 Protein #
38	42	48.8	254	4	AAW66183	AAW66183 Human bon
39	42	48.8	254	4	AAW53797	AAW53797 Human btx
40	42	48.8	254	4	ABG47851	ABG47851 Human liv
41	42	48.8	254	4	AAW01794	AAW01794 Human liv
42	42	48.8	254	5	ABG35833	ABG35833 Human pep
43	42	48.8	679	4	ABG10004	ABG10004 Novel hum
44	42	48.8	1039	3	AAV58837	AAV58837 Soybean c
45	42	48.8	1113	4	ABG10005	ABG10005 Novel hum

ALIGNMENTS

RESULT 1	AAU08777	standard; peptide; 15 AA.
ID	AAU08777	standard; peptide; 15 AA.
XX	AAU08777;	
AC	27-FEB-2002	(first entry)
DT	27-FEB-2002	(first entry)
XX	VE-cadherin N-terminal domain 1 antibody binding peptide #1.	
DE	VE-cadherin; antibody binding peptide; angiogenesis; neoplastic disease;	
XX	VE-cadherin mediated adherens junction formation; autoimmune disease;	
KW	paracellular permeability; solid tumour; collagenous vascular disease;	
KW	rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;	
KW	retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;	
KW	carcinoma; sarcoma; adenocarcinoma; adenosarcoma; adenoma; gene therapy;	
KW	leukaemic tumour; lymphoid tumours; cell proliferation disorder;	
KW	vacuolarisation; blood vessel proliferation disorder; fibrotic disorder;	
KW	age-related muscular degeneration; tumour neovascularisation;	
KW	VE-cadherin N-terminal domain 1.	
XX	Mammalia.	
OS	WO200175109-A2.	
XX	11-OCT-2001.	
XX	30-MAR-2001; 2001WO-US010505.	
XX	31-MAR-2000; 2000US-00540967.	
XX	(IMCL-) IMCLONE SYSTEMS INC.	
XX	Liiao F, Hicklin DJ, Bohlen P;	
XX	WPI: 2001-655988/75.	
XX	New antibody antagonists of VE-cadherin, which does not adversely affect	
PT	vascular permeability, useful for inhibiting angiogenesis or tumor	
PT	metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.	
XX	Claim 1; Page 32; 44pp; English.	
XX	The method relates to an antibody or an antibody fragment, capable of	
CC	specifically binding to a VE-cadherin, and of inhibiting VE-cadherin	
CC	mediated adherens junction formation in vitro, but does not exert any	
CC	significant or substantial effect on paracellular permeability in vitro.	
CC	The antibody or antibody fragment is capable of specifically binding to a	

site on a VE-cadherin within the 5 N-terminal amino acids of domain 1 of a VE-cadherin. The antibody or antibody fragment is useful for inhibiting angiogenesis (e.g. angiogenesis that is associated with a neoplastic disease, a solid tumour, an autoimmune disease, collagenous vascular disease, rheumatoid arthritis, an ophthalmological condition, diabetic retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas, CC adenocarcinomas, adenomas, leukemic tumours or lymphoid tumours). The composition or antibody is also useful for treating a cell proliferation disorder associated with vascularisation (e.g. blood vessel proliferation disorders, fibrotic disorders, angiogenesis, tumour growth, tumour metastasis, rheumatoid arthritis or age-related muscular degeneration). These may also be used for reducing or inhibiting tumour vasculature in a mammal. The nucleic acid that encodes the antibody or is useful in gene therapy, particularly for inhibiting angiogenesis or tumour neovascularisation. This sequence represents a VE-cadherin N-terminal domain 1 antibody binding peptide

SQ Sequence 15 AA:

Query Match	100.0%;	Score 86;	DB 4;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 6.9e-07;		
Matches	15;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY	1 DEIWNOHIDEKNE	15
Dp	1 DEIWNQHIDEKNE	15

RESULT 2
AAU08778
ID AAU08778 standard; peptide; 15 AA.

AC	AAU08778;
XX	
DT	27-FEB-2002 (first entry)

VE-cadherin N-terminal domain 1 antibody binding peptide #2

VE-cadherin; antibody binding peptide; angiogenesis; neoplastic disease;
VE-cadherin mediated adherens junction formation; autoimmune disease;
paracellular permeability; solid tumour; collagenous vascular disease;
rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma
carcinoma; sarcoma; adenocarcinoma; adenoma; gene therapy;
leukaemic tumour; lymphoid tumours; cell proliferation disorder;
vascularisation; blood vessel proliferation disorder; fibrotic disorder;
age-related muscular degeneration; tumour neovascularisation;
VE-cadherin N-terminal domain 1.

Mammalia. OS

PN WO200175109-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US010505.

PR 31-MAR-2000; 2000US-00540967.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Liao F, Hicklin DJ, Bohlen P;

DR WPI; 2001-656988/75.

PT New antibody antagonists of VE-cadherin, which does not adversely affect
PT vascular permeability, useful for inhibiting angiogenesis or tumor
PT metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.

PS Claim 1; Page 32; 44pp; English

The method relates to an antibody or an antibody fragment, capable of

CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
mediated adherens junction formation in vitro, but does not exert any
CC significant or substantial effect on paracellular permeability in vitro.
CC The antibody or antibody fragment is capable of specifically binding to a
CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
CC disease, a solid tumour, an autoimmune disease, collagenous vascular
CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas,
CC adenocarcinomas, adenomas, leukaemic tumours or lymphoid tumours). The
CC composition or antibody is also useful for treating a cell proliferation
CC disorder associated with vascularisation (e.g. blood vessel proliferation
CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
CC These may also be used for reducing or inhibiting tumour vasculature in a
CC mammal. The nucleic acid that encodes the antibody or is useful in gene
CC therapy, particularly for inhibiting angiogenesis or tumour
CC neovascularisation. This sequence represents a VE-cadherin N-terminal
CC domain 1 antibody binding peptide
XX
SQ Sequence 15 AA;
90.7%; Score 78; DB 4; Length 15;
Query Match 90.7%; Pred. No. 1.3e-05;
Best Local Similarity 93.3%;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Sequence 1.5 AA:

Query Match	90.7%;	Score 78;	DB 4;	Length 15;
Best Local Similarity	93.3%;	Pred. No. 1.3e-05;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;

QY	1	DEIWNQMHIDEKNE	15
Db	1	DIWNQMHIDEKNE	15

RESULT 3
AAU08786
ID AAU08786 standard; protein; 103 AA

AC AAU08786;

DT 27-FEB-2002 (first entry)

MURINE VE-CADHERIN N-TERMINAL DOMAIN 1 POLYPEPTIDE

KM VE-cadherin; angiogenesis; neoplastic disease;
 KM VE-cadherin mediated adherens junction formation; autoimmune disease;
 KM paracellular permeability; solid tumour; collagenous vascular disease;
 KM rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
 KM retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma
 KM carcinoma; sarcoma; adenocarcinoma; adenoma; gene therapy;
 KM leukemic tumour; lymphoid tumours; cell proliferation disorder;
 KM vasculatization; blood vessel proliferation disorder; fibrotic disorder;
 KM age-related muscular degeneration; tumour neovascularisation; mouse;
 KM VE-cadherin N-terminal domain 1.

OS Mus sp.

PN WO200175109-A2

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US010505.

PR 31-MAR-2000; 2000US-00540967.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Liao F, Hicklin DJ, Bohlen P;

DR WPI; 2001-656988/75.

PA New antibody antagonists of VE-cadherin, which does not adversely affect
 PR vascular permeability, useful for inhibiting angiogenesis or tumor
 PT metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.

XX Liao F, Hicklin DJ, Bohlen P;
 XX MPI; 2001-656988/75.
 XX
 XX New antibody antagonists of VE-cadherin, which does not adversely affect
 PT vascular permeability; useful for inhibiting angiogenesis or tumor
 PT metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.
 XX
 XX Example 2; Fig 2; 44pp; English.
 XX The method relates to an antibody or an antibody fragment, capable of
 CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
 CC mediated adherens junction formation in vitro, but does not exert any
 CC significant or substantial effect on paracellular permeability in vitro.
 CC The antibody or antibody fragment is capable of specifically binding to a
 CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
 CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
 CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
 CC disease, a solid tumour, an autoimmune disease, collagenous vascular
 CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
 CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
 CC metastasis (e.g. carcinomas, sarcomas, adenocarcinomas, or tumour
 CC adenocarcinomas, adenomas, leukemic tumours or lymphoid tumours). The
 CC composition or antibody is also useful for treating a cell proliferation
 CC disorder associated with vascularisation (e.g. blood vessel proliferation
 CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
 CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
 CC These may also be used for reducing or inhibiting tumour vasculature in a
 CC mammal. The nucleic acid that encodes the antibody or is useful in gene
 CC therapy, particularly for inhibiting angiogenesis or tumour
 CC neovascularisation. This sequence represents a human VE-cadherin N-
 CC terminal domain 1 polypeptide
 XX
 XX Sequence 104 AA;
 SQ
 Query Match 84.9%; Score 73; DB 4; Length 104;
 Best Local Similarity 92.9%; Pred. No. 0.00068;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINWQHIDEKN 14
 | | | | | | | | | | | | | | | |
 Db 1 DWINWQHIDEKN 14

RESULT 6
 ID AAY64578 standard; peptide; 108 AA.
 XX
 AC AAY64578;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Nonclassical cadherin extracellular domain SEQ ID NO:6.
 XX
 XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW 08-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; P8-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease.
 XX
 XX Mammalia.
 OS
 XX
 XX WO957149-A2.
 PN 11-NOV-1999.
 XX
 PD 05-MAY-1999; 99WO-CA000363.
 XX
 PF 05-MAY-1998; 98US-00073040.
 XX
 PR

PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA Blaschuk OW, Gour BJ, Byers S;
 PI MPI; 2000-038791/03.
 XX
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 XX Disclosure; Fig 2; 252pp; English.
 XX
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AA60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention
 XX
 XX Sequence 108 AA;
 SQ
 Query Match 84.9%; Score 73; DB 3; Length 108;
 Best Local Similarity 92.9%; Pred. No. 0.00071;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINWQHIDEKN 14
 | | | | | | | | | | | | | | | |
 Db 5 DWINWQHIDEKN 18

RESULT 7
 ID AAU11276 standard; protein; 566 AA.
 XX
 AC AAU11276;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human recombinant KVE702 polypeptide.
 KW Human; KV protein; KVE702; angiogenic factor antagonist; angiogenesis;
 KW vascular endothelial structure regulator; cancer; vascular endothelium;
 KW tumour; blood vessel; epithelial cell; cytostatic; gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX WO200183562-A2.
 PN 08-NOV-2001.
 XX
 PD 04-MAY-2001; 2001WO-GB001956.
 XX
 PF

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XX 04-MAY-2000; 2000GB-00010630.
XX
XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
XX Jiang WG;
XX
XX WPI; 2002-066521/09.
XX N-PSDB; AAS16965.
XX
XX Novel nucleic acid for inhibition of angiogenesis and prophylaxis or
XX treatment of cancer, comprises both an angiogenic factor antagonist and a
XX vascular endothelial structure regulator.
XX
XX Disclosure; Fig 2; 66pp; English.
XX
XX The invention relates to recombinant nucleic acid sequences that encode
XX both an angiogenic factor antagonist and a vascular endothelial structure
XX regulator, collectively referred to as a KV protein. KV DNA and proteins,
XX and also cells and compositions containing the sequences, are useful in
XX treating or preventing cancer or angiogenesis in mammals, in particular
XX humans. KV proteins are also useful for regulation of the development of
XX blood vessels and their formation, in the vascular endothelium and/or
XX tumour. The KVE702 gene and its fragments are useful in transfection of
XX human epithelial cells and to generate products suitable for angiogenesis
XX intervention. This sequence represents the human KVE702 protein
XX
XX Sequence 566 AA;
XX
XX Query Match      84.9%; Score 73; DB 5; Length 566;
XX Best Local Similarity 92.9%; Pred. No. 0.0044;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 DEINQNMHIDEKN 14
XX | |||||
XX 474 DWIMQNMHIDEKN 487
XX
XX RESULT 8
XX AAU11279
XX ID AAU11279 standard; protein; 594 AA.
XX
XX AC AAU11279;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Human recombinant U37 polypeptide.
XX
XX KM Human; KV protein; KVE702; angiogenic factor antagonist; angiogenesis;
XX vascular endothelial structure regulator; cancer; vascular endothelium;
XX tumour; blood vessel; epithelial cell; cytostatic; gene therapy; U37.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 518
XX FT /note= "Encoded by ATC"
XX
XX PN WO200183562-A2.
XX
XX PD 08-NOV-2001.
XX
XX PF 04-MAY-2001; 2001WO-GB001956.
XX
XX PR 04-MAY-2000; 2000GB-00010630.
XX
XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
XX Jiang WG;
XX
XX WPI; 2002-066521/09.
XX N-PSDB; AAS16975.

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XX XX
XX PT Novel nucleic acid for inhibition of angiogenesis and prophylaxis or
XX treatment of cancer, comprises both an angiogenic factor antagonist and a
XX vascular endothelial structure regulator.
XX
XX PS Disclosure; Fig 15; 66pp; English.
XX
XX The invention relates to recombinant nucleic acid sequences that encode
XX both an angiogenic factor antagonist and a vascular endothelial structure
XX regulator, collectively referred to as a KV protein. KV DNA and proteins,
XX and also cells and compositions containing the sequences, are useful in
XX treating or preventing cancer or angiogenesis in mammals, in particular
XX humans. KV proteins are also useful for regulation of the development of
XX blood vessels and their formation, in the vascular endothelium and/or
XX tumour. The KVE702 gene and its fragments are useful in transfection of
XX human epithelial cells and to generate products suitable for angiogenesis
XX intervention. This sequence represents the human U37 protein used in
XX
XX Sequence 594 AA;
XX
XX Query Match      84.9%; Score 73; DB 5; Length 594;
XX Best Local Similarity 92.9%; Pred. No. 0.0047;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 DEINQNMHIDEKN 14
XX | |||||
XX 49 DWIMQNMHIDEKN 62
XX
XX RESULT 9
XX AAM25634
XX ID AAM25634 standard; protein; 780 AA.
XX
XX AC AAM25634;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-NOV-1997 (first entry)
XX
XX DE Human cadherin-5.
XX
XX KM Human; cadherin; rat; calcium-dependent cell adhesion protein;
XX superfamily; cytoskeleton; eatenin; cancer.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 622
XX FT /note= "encoded by AAG"
XX
XX PN US5646250-A.
XX
XX PD 08-JUL-1997.
XX
XX PF 01-NOV-1994; 94US-00332638.
XX
XX PR 17-APR-1992; 92US-00872643.
XX PR 19-APR-1993; 93US-00049460.
XX
XX (DOHE-) DOHENY EYE INST.
XX
XX Suzuki S;
XX
XX WPI; 1997-362997/33.
XX N-PSDB; AAT85401.
XX
XX Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion.
XX Claim 1; Col 69-72; 56pp; English.
XX
XX This sequence represents human cadherin-5. The invention specifically
XX provides details of human cadherin-5, -8, -11, -12 and -13, and rat
XX cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell

```

CC adhesion proteins. They are glycosylated integral membrane proteins that
 CC have an N-terminal extracellular domain that determines binding
 CC specificity, a hydrophobic membrane spanning region and a C-terminal
 CC cytoplasmic domain, which is highly conserved among members of the
 CC superfamily. The C-terminal domain interacts with the cytoskeleton
 CC through catenins and other cytoskeleton-associated proteins. The novel
 CC cadherin proteins may be used in the analysis of the role of catenins in
 CC various cancers. Sequence analysis of the cadherin proteins also allows
 CC investigation of the structure and function of cadherin. The cadherin
 CC proteins may be isolated by using anti-cadherin antibodies. These
 CC antibodies may also be used to modulate the activity of cadherin and to
 CC determine the tissue specific distribution of cadherin proteins. Each
 CC subclass of cadherins has a unique tissue distribution pattern. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 CC
 CC Sequence 780 AA;
 CC
 CC Query Match 84.9%; Score 73; DB 2; Length 780;
 CC Best Local Similarity 92.9%; Pred. No. 0.0063;
 CC Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 DEINQMHIIDEKN 14
 CC | | | | | | | | | | | | | | | |
 CC 44 DWIMQMHIIDEKN 57
 CC
 CC Db
 CC
 CC RESULT 10
 CC AAM13130
 CC ID AAM13130 standard; protein; 780 AA.
 CC XX
 CC AC AAM13130;
 CC XX
 CC DT 25-MAR-2003 (revised)
 CC DT 13-MAY-1997 (first entry)
 CC XX
 CC DE Full length human cadherin-5.
 CC XX
 CC KW Ca2+ dependent; cell adhesion protein; placental; cadherin; rat; brain;
 CC KW human; antibody; purification; determination; tissue expression;
 CC KW binding antagonist; calcium ion.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC PN US5597725-A.
 CC XX
 CC PD 28-JAN-1997.
 CC XX
 CC PF 26-JAN-1994; 94US-00188228.
 CC XX
 CC PR 17-APR-1992; 92US-00872643.
 CC PR 19-APR-1993; 93US-00049460.
 CC XX
 CC PA (DOHE-) DOHENY EYE INST.
 CC XX
 CC PI Suzuki S;
 CC XX
 CC DR WPI; 1997-108328/10.
 CC DR N-PSDB; AAT61921.
 CC XX
 CC PT Antibodies to cadherin proteins - useful as cadherin antagonists, etc.
 CC XX
 CC PS Claim 5; Col 75-78; 59pp; English.
 CC XX
 CC The present sequence is full length human cadherin-5, which is a Ca2+
 CC dependent cell adhesion protein. The human cadherin cDNA was isolated
 CC from a placental cDNA library, using probes based on homologous rat
 CC cadherin cDNA. Antibodies or fragments that specifically bind the human
 CC cadherin can be used to purify the cadherin, determine its tissue
 CC expression and antagonise its ligand/antiligand binding activities.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 CC Sequence 780 AA;
 CC
 CC SQ

Query Match 84.9%; Score 73; DB 2; Length 780;
 Best Local Similarity 92.9%; Pred. No. 0.0063;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DEINQMHIIDEKN 14
 | | | | | | | | | | | | | | | |
 Db 44 DWIMQMHIIDEKN 57
 RESULT 11
 ABB81477
 ID ABB81477 standard; protein; 784 AA.
 XX
 AC ABB81477;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Human VE-cadherin protein SEQ ID NO:52.
 XX
 KW Cadherin; alpha-catenin; cancer; beta-catenin binding domain; melanoma;
 KW o-catenin; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN US2002045591-A1.
 XX
 PD 18-APR-2002.
 XX
 PF 17-JUL-2001; 2001US-00905983.
 XX
 PR 26-MAY-1998; 98IL-00124650.
 PR 26-MAY-1999; 99US-00318633.
 XX
 PA (GEIG/) GEIGER B.
 PA (BENZ/) BEN-ZE'EV A.
 PA (SADO/) SADOT E.
 XX
 PI Geiger B, Ben-Ze'ev A, Sadot E;
 XX
 DR WPI; 2002-499105/53.
 DR N-PSDB; ABN89394.
 XX
 PT New construct encoding soluble cytoplasmic portion of cadherin including
 PT beta catenin binding domain useful in treating cancer associated with
 PT high beta-catenin activity e.g. colon cancer and melanoma.
 XX
 PS Example 3; Page 56-58; 102pp; English.
 XX
 CC The present invention describes a pharmaceutical composition for treating
 CC cancer associated with abnormally high beta-catenin activity. The
 CC pharmaceutical composition comprises a gene therapy vehicle harbouring a
 CC polynucleotide that contains: (i) a nucleotide sequence encoding a
 CC soluble cytoplasmic portion of a cadherin which lacks a transmembrane
 CC portion and an extracellular portion of the cadherin, and includes a beta
 CC -catenin binding domain; and (b) an upstream promoter for directing
 CC expression of the soluble cytoplasmic portion of the cadherin in a
 CC mammalian cell. Also described is a pharmaceutical composition for
 CC treating cancer associated with abnormally high activity levels of beta-
 CC catenin comprising a gene therapy vehicle harbouring a polynucleotide
 CC that contains: (a) a nucleotide sequence encoding an o-catenin; and (b)
 CC an upstream promoter for directing expression of the o-catenin in a
 CC mammalian cell. The pharmaceutical compositions have cytostatic activity
 CC and can be used in the suppression of beta-catenin-mediated
 CC transactivation. They can be used for treating cancers associated with
 CC abnormally high activity levels of beta-catenin such as colon cancers and
 CC melanomas, by reducing these high activity levels of beta-catenin in
 CC mammalian cells. The present sequence represents human VE-cadherin which
 CC is used in the exemplification of the present invention
 CC
 CC Sequence 784 AA;
 CC
 CC SQ
 CC Query Match 84.9%; Score 73; DB 5; Length 784;
 CC Best Local Similarity 92.9%; Pred. No. 0.0064;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEIMNQMHIDEKN 14
| | | | | | | | | | | | | | | |
48 DWIMNQMHIDEKN 61

RESULT 12
ID ABU03507
ABU03507 standard; protein; 784 AA.
XX
AC ABU03507;
XX
DT 21-JAN-2003 (first entry)
XX
DE Angiogenesis-associated human protein sequence #52.
XX
KW Human; angiogenesis-associated transcript; angiogenesis;
KW angiogenesis-associated disease; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200279492-A2.
XX
PD 10-OCT-2002.
XX
PF 14-FEB-2002; 2002WO-US004915.
XX
PR 14-FEB-2001; 2001US-00784356.
PR 22-FEB-2001; 2001US-00791390.
PR 19-APR-2001; 2001US-0285475P.
PR 03-AUG-2001; 2001US-0310025P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334244P.
XX
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Murray R, Glynn R, Watson SR, Aziz N;
XX
DR WPI; 2003-040681/03.
XX
DR N-PSDB; ABX08791.
XX
XX
PT Detecting angiogenesis-associated transcript in a cell for diagnosing and
PT treating cancer by contacting a sample with a polynucleotide that
PT exhibits changes in expression level as a function of time in tissue
XX
XX undergoing angiogenesis.
XX
PS Example 2; Page 230; 291pp; English.
XX
CC The present invention relates to methods and compositions for detecting
CC an angiogenesis-associated transcript in a cell in a patient. The method
CC involves contacting a biological sample from the patient with a
CC polynucleotide that selectively hybridizes to a sequence at least 80%
CC identical to any of the angiogenesis-associated human polynucleotide
CC sequences given in the specification. These angiogenesis-associated
CC polynucleotide sequences comprise genes that exhibit changes in
CC expression levels as a function of time in tissue undergoing
CC angiogenesis. The method and the polynucleotide sequences of the
CC invention are useful for diagnosing and treating angiogenesis and
CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
CC sequences are also useful in the gene therapy of such disorders. The
CC angiogenesis-associated proteins encoded by the polynucleotide sequences
CC are useful as a vaccine for therapeutic and prophylactic immunisation.
CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences
XX
SQ Sequence 784 AA;

Query Match 84.9%; Score 73; DB 6; Length 784;
Best Local Similarity 92.9%; Pred. No. 0.0064;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEIMNQMHIDEKN 14
| | | | | | | | | | | | | | | |

DB 48 DWIMNQMHIDEKN 61

RESULT 13
ID ABUS6570
ABUS6570 standard; protein; 784 AA.
XX
AC ABUS6570;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #163.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0288470P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
XX
DR N-PSDB; ABX76299.
XX
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
XX
XX expression in lung cancer.
XX
PS Claim 27; Page 314; 453pp; English.
XX
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX
XX invention
SQ Sequence 784 AA;

Query Match 84.9%; Score 73; DB 6; Length 784;
Best Local Similarity 92.9%; Pred. No. 0.0064;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEINQMHIIDEKN 14
 DB 48 DWINQMHIIDEKN 61

RESULT 14
 ADA03363
 ID ADA03363 standard; protein; 784 AA.
 AC ADA03363;
 XX
 DE 06-NOV-2003 (first entry)
 XX
 DE Human vascular endothelial cadherin protein.
 XX
 KW cytostratic; antidiabetic; ophthalmological; antiarthritic;
 KM endostatin receptor; angiogenesis inhibitor; human;
 KW vascular endothelial cadherin; angiogenesis; blood vessel; cancer;
 KW diabetic retinopathy; rheumatoid arthritis; receptor.
 XX
 OS Homo sapiens.
 XX
 PN MO2003038096-A1.
 PD 08-MAY-2003.
 PF 28-OCT-2002; 2002WO-JP011143.
 PR 30-OCT-2001; 2001JP-00333295.
 PA (KUBO/) KUBOTA S.
 PA (NEMO/) NEMOTO T.
 XX
 PI Kubota S, Nemoto T;
 XX
 DR WPI; 2003-430528/40.
 DR N-PSDB; ADA03362.
 XX
 PT Vascular endothelial cadherin is a receptor to endostatin for screening
 PT endostatin agonists and antagonists as angiogenesis inhibitors and
 PT remedies for cancer development and proliferation.
 PS Claim 2; Page 44-47; 56pp; Japanese.
 XX
 CC The invention relates to a DNA encoding an endostatin receptor protein
 CC (human vascular endothelial (VE) cadherin (1)) or its partial peptides or
 CC encoding a protein derived from (1) by addition, deletion or substitution
 CC of one or more amino acid residues and having similar binding activity to
 CC endostatin. The sequence can be used in the regulation of angiogenesis in
 CC the treatment and prevention of diseases associated with the formation of
 CC new blood vessels, including cancer, cancer proliferation, diabetic
 CC retinopathy and rheumatoid arthritis. This sequence corresponds to the VE
 CC cadherin protein which serves as an endostatin receptor protein.
 XX
 SQ Sequence 784 AA;
 QY Query Match 84.9%; Score 73; DB 6; Length 784;
 Best Local Similarity 92.9%; Pred. No. 0.0064;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
 ABB49545
 ID ABB49545 standard; protein; 77 AA.
 AC ABB49545;
 XX
 DT 05-FEB-2002 (first entry)

XX
 DE Listeria monocytogenes protein #2249.
 XX
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 PN MO200177335-A2.
 PD 18-OCT-2001.
 PF 11-APR-2001; 2001WO-FR001118.
 PR 11-APR-2000; 2000FR-00004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangoul L, Couve E, Rusniok C, Felhi H, Deboux P;
 PI Dussurget O, Chetoui F, Nedjati H, Glaser P, Kunst F, Coesart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tietzer-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Maduenio E, De Pablo B, Weiland U, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voess H;
 XX
 DR WPI; 2002-010914/01.
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and related
 PT polypeptides.
 PS Claim 6; SEQ ID NO 2250; 192pp; French.
 XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in L.
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present invention is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of L. monocytogenes and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate L. monocytogenes-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccines compositions for the treatment or prevention of infections by L.
 CC monocytogenes and related organisms. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 77 AA;
 QY Query Match 58.1%; Score 50; DB 5; Length 77;
 Best Local Similarity 53.3%; Pred. No. 2.2;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

DB 62 DELMDAYLIDEKNK 76

Search completed: July 29, 2004, 11:34:52
 Job time : 48.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:37:16 ; Search time 38.333 Seconds

(Without alignments)
122.745 Million cell updates/sec

Title: US-10-040-128-2

Sequence: 1 DWIMNQMHIIDEKNE 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 segs, 313682936 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	15	US-10-040-128-2	Sequence 2, Appl1
2	87	94.6	15	US-10-040-128-3	Sequence 3, Appl1
3	87	94.6	108	US-10-006-869-6	Sequence 6, Appl1
4	87	94.6	108	US-10-395-032-6	Sequence 6, Appl1
5	87	94.6	784	US-09-905-983-52	Sequence 52, Appl1
6	87	94.6	784	US-10-211-462-105	Sequence 105, Appl1
7	87	94.6	784	US-10-021-660-99	Sequence 99, Appl1
8	87	94.6	784	US-10-174-677-23	Sequence 23, Appl1
9	87	94.6	15	US-10-040-128-1	Sequence 1, Appl1
10	52	56.5	167	US-10-243-552-596	Sequence 596, App
11	52	56.5	772	US-09-978-295A-264	Sequence 264, App
12	52	56.5	772	US-09-978-687-264	Sequence 264, App
13	52	56.5	772	US-09-978-182A-264	Sequence 264, App
14	52	56.5	772	US-09-999-832A-264	Sequence 264, App
15	52	56.5	772	US-09-978-189-264	Sequence 264, App

16	52	56.5	772	10	US-09-978-608A-264	Sequence 264, App
17	52	56.5	772	10	US-09-978-585A-264	Sequence 264, App
18	52	56.5	772	10	US-09-978-193A-264	Sequence 264, App
19	52	56.5	772	10	US-09-978-403A-264	Sequence 264, App
20	52	56.5	772	10	US-09-978-564A-264	Sequence 264, App
21	52	56.5	772	10	US-09-999-833A-264	Sequence 264, App
22	52	56.5	772	10	US-09-981-915A-264	Sequence 264, App
23	52	56.5	772	10	US-09-978-824-264	Sequence 264, App
24	52	56.5	772	10	US-09-918-585A-264	Sequence 264, App
25	52	56.5	772	10	US-09-978-423A-264	Sequence 264, App
26	52	56.5	772	10	US-09-978-187B-264	Sequence 264, App
27	52	56.5	772	10	US-09-999-830A-264	Sequence 264, App
28	52	56.5	772	10	US-09-978-757A-264	Sequence 264, App
29	52	56.5	772	10	US-09-978-643A-264	Sequence 264, App
30	52	56.5	772	10	US-09-978-375A-264	Sequence 264, App
31	52	56.5	772	10	US-09-978-188A-264	Sequence 264, App
32	52	56.5	772	10	US-09-978-194A-264	Sequence 264, App
33	52	56.5	772	10	US-09-978-802A-264	Sequence 264, App
34	52	56.5	772	10	US-09-978-829A-264	Sequence 264, App
35	52	56.5	772	10	US-09-978-654A-264	Sequence 264, App
36	52	56.5	772	10	US-09-978-665A-264	Sequence 264, App
37	52	56.5	772	10	US-09-978-823A-264	Sequence 264, App
38	52	56.5	772	10	US-09-978-544A-264	Sequence 264, App
39	52	56.5	772	10	US-09-978-802A-264	Sequence 264, App
40	52	56.5	772	10	US-10-164-749A-264	Sequence 264, App
41	52	56.5	772	12	US-10-206-915-106	Sequence 106, App
42	52	56.5	772	12	US-10-199-670-106	Sequence 106, App
43	52	56.5	772	12	US-10-201-858-106	Sequence 106, App
44	52	56.5	772	12	US-09-999-831A-264	Sequence 264, App
45	52	56.5	772	12	US-09-999-831A-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-10-040-128-2
; Sequence 2, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang
; APPLICANT: Hicklin, Daniel J.
; TITLE OF INVENTION: Antibody Antagonists of V6-Cadherin Without Adverse Effects on
; TITLE OF INVENTION: Vascular Permeability
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-2

Query Match
Best Local Similarity 100.0%; Score 92; DB 13; Length 15;
Matches 15; Conservative 0; Pred. No. 1.2e-06;
Mismatch 0; Indels 0; Gaps 0;

QY 1 DWIMNQMHIIDEKNE 15
|||
DB 1 DWIMNQMHIIDEKNE 15

RESULT 2
US-10-040-128-3
; Sequence 3, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang

```
; APPLICANT: Hicklin, Daniel J.
; APPLICANT: Bohlen, Peter
; TITLE OF INVENTION: Antagonists of VE-Cadherin Without Adverse Effects on
; TITLE OF INVENTION: Vascular Permeability
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-3

Query Match          94.6%; Score 87; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  DWIMNQMHIDEKN 14
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Db      1  DWIMNQMHIDEKN 14

RESULT 3
US-10-006-869-6
; Sequence 6, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-869-6

Query Match          94.6%; Score 87; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  DWIMNQMHIDEKN 14
        |||||
Db      5  DWIMNQMHIDEKN 18

RESULT 4
US-10-395-032-6
; Sequence 6, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-395-032-6

Query Match          94.6%; Score 87; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  DWIMNQMHIDEKN 14
        |||||
Db      5  DWIMNQMHIDEKN 18

RESULT 5
US-09-905-983-52
; Sequence 52, Application US/09905983
; Patent No. US20020045591A1
; GENERAL INFORMATION:
; APPLICANT: Geisler, Benjamin
; APPLICANT: Ben-Ze'ev, Avri
; APPLICANT: Sadot, Eliaht
; TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
; FILE REFERENCE: 01/22326
; CURRENT APPLICATION NUMBER: US/09/905,983
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-983-52

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Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  DWIMNQMHIDEKN 14
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Db      48 DWIMNQMHIDEKN 61

RESULT 6
US-10-211-462-105
; Sequence 105, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-105
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Query Match 94.6%; Score 87; DB 12; Length 784;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWINQMHIDEKN 14
|||||
Db 48 DWINQMHIDEKN 61

RESULT 7

US-10-021-660-99
; Sequence 99, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Guyne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: ROS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; FILE REFERENCE: 018501-00071005
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-99

Query Match 94.6%; Score 87; DB 14; Length 784;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWINQMHIDEKN 14
|||||
Db 48 DWINQMHIDEKN 61

RESULT 8

US-10-174-677-23
; Sequence 23, Application US/10174677
; Publication No. US20030190704A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Ting
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANCHORING STEM CELLS IN A MICROENVIR
; FILE REFERENCE: 40716(IP-012)
; CURRENT APPLICATION NUMBER: US/10/174,677
; CURRENT FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-677-23

Query Match 94.6%; Score 87; DB 14; Length 784;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWINQMHIDEKN 14
|||||
Db 48 DWINQMHIDEKN 61

RESULT 9

US-10-040-128-1
; Sequence 1, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang
; APPLICANT: Hicklin, Daniel J.
; APPLICANT: Bohlen, Peter
; TITLE OF INVENTION: Antibody Antagonists of VE-Cadherin Without Adverse Effects on
; TITLE OF INVENTION: Vascular Permeability
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-1

Query Match 84.8%; Score 78; DB 13; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DWINQMHIDEKNE 15
|||||
Db 1 DWINQMHIDEKNE 15

RESULT 10
US-10-243-552-596
; Sequence 596, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Ma, Yunding
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 8077A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: PC_FL_genes Version 5.0
; SEQ ID NO 596
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-243-552-596

Query Match 56.5%; Score 52; DB 12; Length 167;
Best Local Similarity 53.8%; Pred. No. 7.2;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WNNQNHIDEKN 14
Db 45 WNNQFVPEEMN 57

RESULT 11

US-09-978-295A-264
Sequence 264, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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Query Match 56.5%; Score 52; DB 9; Length 772;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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Db 45 WYWNQFVPEEMN 57

RESULT 12
US-09-978-697-264
Sequence 264, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavins, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR APPLICATION NUMBER: 2001-10-16
PRIOR FILING DATE: 2001-07-30
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Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P109
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Query Match          56.5%; Score 52; DB 9; length 772;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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; Sequence 264, Application US/0999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
```

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; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Rong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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42	PRIOR APPLICATION NUMBER: 60/0856977

Query Match	56.5%	Score 52;	DB 9;	Length 772;
Best Local Similarity	53.8%;	Pred. No. 31;		
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Db	45	W	V	W	N	Q	F	V	P	E	E	M	N	57

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US-09-978-189-264
Sequence 264, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kjavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Title: US-10-040-128-2

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	87	94.6	780	1	US-08-188-228-50
5	87	94.6	780	1	US-08-332-643-44
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ALIGNMENTS

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; Patent No. 6358920
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; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.40701
; CURRENT APPLICATION NUMBER: US/09/167, 859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-859-6

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Db 5 DWIMNQHIDEKNE 18

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; Sequence 6, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.40701
; CURRENT APPLICATION NUMBER: US/09/839, 542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
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US-09-839-542B-6

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 5 DWIMNQHIDEKN 18

RESULT 3

US-09-535-852-6
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; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-535-852-6

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 5 DWIMNQHIDEKN 18

RESULT 4

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; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
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; FILING DATE: 19 APR 1993
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; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-50

Query Match 94.6%; Score 87; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 3,8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMNQHIDEKN 14
|||||
DB 44 DWIMNQHIDEKN 57

RESULT 5

US-08-332-643-44
; Sequence 44, Application US/08332643
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-643-44

Query Match 94.6%; Score 87; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 3,8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMNQHIDEKN 14
|||||

Db 44 DWINQMHIDEKN 57

```
RESULT 6
US-08-332-638-50
; Sequence 50, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-50
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```
Query Match 94.6%; Score 87; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DWINQMHIDEKN 14
|:|||||:|
Db 44 DWINQMHIDEKN 57
```

```
RESULT 7
US-09-187-859-13
; Sequence 13, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
```

```
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-859-13
```

```
Query Match 53.3%; Score 49; DB 4; Length 110;
Best Local Similarity 63.6%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2 WWINQMHIDE 12
|:|||||:|
Db 6 WWINQMFVLEE 16
```

```
RESULT 8
US-09-839-542B-13
; Sequence 13, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-13
```

```
Query Match 53.3%; Score 49; DB 4; Length 110;
Best Local Similarity 63.6%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 WWINQMHIDE 12
|:|||||:|
Db 6 WWINQMFVLEE 16
```

```
RESULT 9
US-09-535-852-13
; Sequence 13, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-852-13
```

```
Query Match 53.3%; Score 49; DB 4; Length 110;
Best Local Similarity 63.6%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 WWINQMHIDE 12
|:|||||:|
Db 6 WWINQMFVLEE 16
```

RESULT 10
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 53.3%; Score 49; DB 1; Length 532;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 MINOMHIDE 12
Db 63 WWMQMFVLEE 73

RESULT 11
US-08-332-638-44
Sequence 44, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 564625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 53.3%; Score 49; DB 1; Length 532;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 MINOMHIDE 12
Db 63 WWMQMFVLEE 73

RESULT 12
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 53.3%; Score 49; DB 1; Length 793;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
|:|||||: ||
56 WWINOMFVLEE 66

RESULT 13

US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 53.3%; Score 49; DB 1; Length 793;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 WINNOMHIDE 12
|:|||||: ||

Db 56 WWINOMFVLEE 66

RESULT 14

US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 53.3%; Score 49; DB 1; Length 793;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
|:|||||: ||
Db 56 WWINOMFVLEE 66

RESULT 15

US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 53.3%; Score 49; DB 1; Length 799;
Best Local Similarity 63.6%; Pred. NO. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WNNQMHIDE 12
|:|||||:|
Db 63 WNNQMFVLEE 73

Search completed: July 29, 2004, 11:38:39
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:30:55 ; Search time 31 Seconds

(Without alignments)
152.670 Million cell updates/sec

Title: US-10-040-128-2
Perfect score: 92
Sequence: 1 DWIMQNHIDEKNE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	94.6	782	6 Q8WNW5	Q8WNW5 sus scrofa
2	64	63.6	773	13 Q8AYD0	Q8AYD0 gallus galli
3	50	53.3	524	5 O01321	O01321 caenorhabdi
4	49	53.3	247	11 Q8C9N7	Q8C9N7 mus musculu
5	49	53.3	716	11 Q8C449	Q8C449 mus musculu
6	49	53.3	716	11 Q8C375	Q8C375 mus musculu
7	49	53.3	754	11 Q8BRK4	Q8BRK4 mus musculu
8	47	51.1	333	2 Q9L3G9	Q9L3G9 erwina rna
9	46	50.0	313	16 Q88HL3	Q88HL3 pseudomonas
10	46	50.0	839	5 Q9N2R2	Q9N2R2 strongyloce
11	46	50.0	1497	16 Q87GE0	Q87GE0 vibrio para
12	45.5	49.5	143	5 Q9V1E8	Q9V1E8 dirosophila
13	45	48.9	176	10 Q8RYE1	Q8RYE1 arena strig
14	45	48.9	241	4 Q8ET58	Q8ET58 homo sapien
15	45	48.9	241	5 Q8IK72	Q8IK72 plasmodium
16	45	48.9	310	10 Q8W5G3	Q8W5G3 oryza sativ

17	45	48.9	350	3 Q00870	Q00870 nectria hae
18	45	48.9	391	16 Q31773	Q31773 bacillus su
19	45	48.9	493	4 Q96L07	Q96L07 homo sapien
20	45	48.9	522	4 Q96DN1	Q96DN1 homo sapien
21	45	48.9	522	4 Q86DB6	Q86DB6 homo sapien
22	45	48.9	522	11 Q8X377	Q8X377 mus musculu
23	45	48.9	781	4 Q86UP1	Q86UP1 homo sapien
24	45	48.9	794	13 Q93264	Q93264 xenopus lae
25	45	48.9	796	4 Q96CZ9	Q96CZ9 homo sapien
26	45	48.9	796	11 Q8C7Q6	Q8C7Q6 mus musculu
27	45	48.9	819	4 Q86UP0	Q86UP0 homo sapien
28	45	48.9	1356	5 Q8ICG0	Q8ICG0 plasmodium
29	44.5	48.4	963	10 Q9STU7	Q9STU7 arabidopsis
30	44	47.8	76	11 Q8BLT5	Q8BLT5 mus musculu
31	44	47.8	163	16 Q99S13	Q99S13 staphylococ
32	44	47.8	164	2 Q9ZAH7	Q9ZAH7 staphylococ
33	44	47.8	219	16 Q8ECK3	Q8ECK3 shewanella
34	44	47.8	337	11 Q8BLB5	Q8BLB5 mus musculu
35	44	47.8	340	11 Q8BLT4	Q8BLT4 mus musculu
36	44	47.8	500	16 Q99T97	Q99T97 staphylococ
37	44	47.8	500	16 Q8NW11	Q8NW11 staphylococ
38	44	47.8	551	13 Q8AWW2	Q8AWW2 gallus galli
39	44	47.8	558	5 Q20375	Q20375 caenorhabdi
40	44	47.8	586	5 Q95ZT7	Q95ZT7 caenorhabdi
41	44	47.8	630	4 Q81Y78	Q81Y78 homo sapien
42	44	47.8	785	11 Q8BM92	Q8BM92 mus musculu
43	44	47.8	790	4 Q8N522	Q8N522 homo sapien
44	44	47.8	790	4 Q91838	Q91838 xenopus lae
45	44	47.8	794	4 Q86UD2	Q86UD2 homo sapien

ALIGNMENTS

RESULT 1

Q8WNW5
ID Q8WNW5
AC Q8WNW5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VB cadherin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
BN [1]
RP SEQUENCE FROM N.A.
RA Hirano M., Hirano K., Nishimura J., Kanaide H.;
RT "Transcriptional up-regulation of p27Kip1 during contact-induced
RT growth arrest in the endothelial cells."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99119339; PubMed=9918866;
RA Hirano M., Niiro N., Hirano K., Nishimura J., Harshehorn D.J.,
RA Kanaide H.;
RT "Expression, subcellular localization and cloning of the 130 kDa
RT regulatory subunit of myosin phosphatase in porcine aortic endothelial
RL cells."
RL Biochem. Biophys. Res. Commun. 254:490-496(1999).
CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
CC -!- THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
CC SORTING OF HETEROGENEOUS CELL TYPES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL, AB046120; BAB82983.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.

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DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; cadherin_5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN-
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS00268; CADHERIN_2; 5.
DR KEGG; Calcium-binding; Cell adhesion; Glycoprotein.
KW SEQUENCE 782 AA; 87536 MW; 6E1D12D017CB1083 CRC64;
SQ
Query Match 94.6%; Score 87; DB 6; Length 782;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DWIMNOMHIDEKN 14
Db 45 DWIMNOMHIDEKN 58
RESULT 2
Q8AYD0 PRELIMINARY; PRT; 773 AA.
ID 08AYD0;
AC 08AYD0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Vascular endothelial cadherin precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Romero S., Jaffredo T., Dunon D.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF522067; AAN33002.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; cadherin_5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS00268; CADHERIN_2; 5.
DR KEGG; Calcium-binding; Cell adhesion; Glycoprotein.
KW SIGNAL.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 43 773 VASCULAR ENDOTHELIAL CADHERIN.
SQ SEQUENCE 773 AA; 86842 MW; ACS9CEH1119043F4 CRC64;
Query Match 69.6%; Score 64; DB 13; Length 773;
Best Local Similarity 83.3%; Pred. No. 0.085;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DWIMNOMHIDEKN 12
Db 41 DWIMNOMHIDEKN 52
RESULT 3
Q01321 PRELIMINARY; PRT; 524 AA.
ID 001321;
AC 001321; P91858;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE F26H9.1 protein.
DE F26H9.1.
GN F26H9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

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OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Boulfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gaxton A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R., Smaison N., Smith A., Sonhammer E., Straden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Woldman F., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Sims M.;
RL EMBL; 281516; CAB04206.1; -.
DR EMBL; 275535; CAB04206.1; JOINED.
DR EMBL; 275535; CAB99829.1; -.
DR EMBL; 281516; CAB99829.1; JOINED.
DR PIR; T20872; T20872.
DR WormPep; F26H9.1; CE09706.
DR InterPro; IPR008945; SKP1_Skp2.
SQ SEQUENCE 524 AA; 60462 MW; 6A85B0CDDC0D2B76 CRC64;
Query Match 54.3%; Score 50; DB 5; Length 524;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 WIMNOMHIDEKN 15
Db 486 WIMNOMHIDEKN 499
RESULT 4
Q8C9N7 PRELIMINARY; PRT; 247 AA.
ID 08C9N7;
AC 08C9N7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cadherin 8.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK041720; BAC31041.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin_2.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 1.

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DR PROSITE; PS00232; CADHERIN 1; 1.
 DR PROSITE; PS50268; CADHERIN 2; 2.
 SQ SEQUENCE 247 AA; 27565 MW; DF7551A97A29289D CRC64;

Query Match
 Best Local Similarity 53.3%; Score 49; DB 11; Length 247;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 W1WNOHIDE12
 Db 63 W1WNOHIDE12 73

RESULT 5
 Q8C449 PRELIMINARY; PRT; 716 AA.

AC Q8C449; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cadherin 8.
 GN CDH8.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK083092; BAC38758.1; -.
 DR MGD; MGI:107434; Cdh8.

DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF01049; Cadherin_C; 5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.

DR PROSITE; PS00232; CADHERIN 1; 3.
 DR PROSITE; PS50268; CADHERIN 2; 5.
 SQ SEQUENCE 716 AA; 79145 MW; 976F5D845F938BD CRC64;

Query Match
 Best Local Similarity 53.3%; Score 49; DB 11; Length 716;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 W1WNOHIDE12
 Db 63 W1WNOHIDE12 73

RESULT 6
 Q8C375 PRELIMINARY; PRT; 716 AA.

AC Q8C375; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cadherin 8.
 GN CDH8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK086711; BAC39724.1; -.
 DR MGD; MGI:107434; Cdh8.

DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.

DR PROSITE; PS00232; CADHERIN 1; 3.
 DR PROSITE; PS50268; CADHERIN 2; 5.
 SQ SEQUENCE 716 AA; 79149 MW; 5BBD598F6638624A CRC64;

Query Match
 Best Local Similarity 53.3%; Score 49; DB 11; Length 716;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 W1WNOHIDE12
 Db 63 W1WNOHIDE12 73

RESULT 7
 Q8BRK4 PRELIMINARY; PRT; 754 AA.

AC Q8BRK4; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cadherin 8.
 GN Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK044046; BAC31751.1; -.

DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.

DR PROSITE; PS00232; CADHERIN 1; 3.
 DR PROSITE; PS50268; CADHERIN 2; 5.
 SQ SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;

Query Match
 Best Local Similarity 53.3%; Score 49; DB 11; Length 754;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 W1WNOHIDE12
 Db 63 W1WNOHIDE12 73

Db 63 WVMNQMFVLEE 73

RESULT 8

Q9L3G9 PRELIMINARY; PRT; 333 AA.

AC Q9L3G9; (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DT 01-OCT-2000 (TREMBLrel. 25, last annotation update)

DE Endoglucanase precursor (EC 3.2.1.4).

GN CELA

OS Erwina rhapontici.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Erwina.

OX NCBI_TaxID=55212;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCPPB2989;

RA Saarihahti H.T.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NCPPB2989;

RA Riekkilä R.;

RT "Members of the amylovora group of Erwina are cellulytic and possess genes homologous to the type II secretion pathway."

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ276358; CAB89803.1; -

DR GO; GO:0008810; P:cellulase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR002037; Glyco_hydro_8.

DR InterPro; IPR008928; Glyco_trans_6hp.

DR Pfam; PF01270; Glyco_hydro_8; 1.

DR PRINTS; PRO0735; GLHYDRLAS8.

KW Glycosidase; Hydrolase; Signal.

FT SIGNAL 1 23

FT CHAIN 24 333

FT SEQUENCE 333 AA; 37784 MW; D75CF212302673A CRC64;

QY Query Match 51.1%; Score 47; DB 2; Length 333; Best Local Similarity 42.9%; Pred. No. 20; Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 2 WVMNQMHIDEKNE 15

Q88HL3 PRELIMINARY; PRT; 313 AA.

AC Q88HL3; (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, last sequence update)

DT 01-JUN-2003 (TREMBLrel. 25, last annotation update)

DE Nickel ABC transporter, permease protein.

GN NIKB OR PP3343.

OS Pseudomonas putida (strain KT2440).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=160486;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=22423060; PubMed=12534463;

RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty J., Khouri H., Hance I., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Mazzei A., Utecher T., Rizzo M., Lee K., Kosack D., Westl D., Wedler H., lauber J., Stjepandic D., Hohensel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tümmeler B.,

RA Fraser C.M.;

RT "Complete genome sequence and comparative analysis of the metabolically versatile *Pseudomonas putida* KT2440."

RL Environ. Microbiol. 4:799-808 (2002).

DR EMBL; AE016786; AAN68947.1; -

DR TIGR; PP3343; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF00528; BPD_transp; 1.

KW Complete proteome.

FT SEQUENCE 313 AA; 34571 MW; 048CD2BBE53F87C CRC64;

QY Query Match 50.0%; Score 46; DB 16; Length 313; Best Local Similarity 42.9%; Pred. No. 27; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 71 WVMNVAHLD 79

Q9N2R2 PRELIMINARY; PRT; 839 AA.

AC Q9N2R2; (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)

DE Krox1 protein.

OS Strongylocentrotus purpuratus (Purple sea urchin).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Echinozoidea; Echinoidae; Echinoida; Strongylocentrotidae;

OC Strongylocentrotus.

OX NCBI_TaxID=7668;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=97177555; PubMed=9025071;

RA Wang W., Mikhramanaye A.H., Gonzalez-Rimbau M., Vlahou A., Flytzanis C.N., Klein W.H.;

RT "Very early and transient vegetal-plate expression of SpKrox1, a Kruppel/krox gene from Strongylocentrotus purpuratus."

RL Mech. Dev. 60:185-195 (1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Wang W.;

RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -i- SIMILARITY: CONTAINS 1 SET DOMAIN.

DR EMBL; AF102558; AAF30407.1; -

DR HSSP; P08048; 7ZNF.

DR InterPro; IPR001214; SET.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF00856; SET; 1.

DR Pfam; PF00096; ZF_C2H2; 4.

DR ProDom; PD000003; Znf_C2H2; 1.

DR SMART; SM00317; SET; 1.

DR SMART; SM00355; ZNF_C2H2; 4.

DR PROSITE; PS50280; SET; 1.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

KW Metal-binding; Zinc; Zinc-finger.

FT SEQUENCE 839 AA; 95305 MW; ADEE53AD63F53953 CRC64;

QY Query Match 50.0%; Score 46; DB 5; Length 839; Best Local Similarity 42.9%; Pred. No. 76; Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 749 WIMRIEINQENK 762

RESULT 11

Q87GE0 PRELIMINARY; PRT; 1497 AA.
 AC 087GE0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Conserved hypothetical protein.
 GN VPAl376.
 OS *Vibrio parahaemolyticus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxId=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMD 221063 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 distance from that of *V. cholerae*.";
 RL Lancet 361:743-749 (2003).
 DR EMBL; AP005088; BAC62719.1; -;
 DR InterPro; IPR000437; Prok_lipoprot.S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 1497 AA; 165870 MW; 7EFB28D11BD8DB CRC64;

Query Match 50.0%; Score 46; DB 16; Length 1497;
 Best Local Similarity 43.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 2 WTWQNMH--IDEKNE 15
 Db 935 WLMNDLRYSYDQEKND 950

RESULT 12

Q9YV168 PRELIMINARY; PRT; 143 AA.
 AC 09YV168;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG14611 protein.
 GN PERI OR BCDNA;RH30329 OR CG10066 OR CG14611.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baker E.G., Helt G., Nelson C.R., Makios G.L.G.,
 RA Abirl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baas A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Butkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner M.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Kaspen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munzy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 DR EMBL; AE003672; AAF54057.1; -;
 DR FLYBASE; Fggn037475; Fer1.
 SQ SEQUENCE 143 AA; 16081 MW; 6A8B602464FA4D7E CRC64;

Query Match 49.5%; Score 45.5; DB 5; Length 143;
 Best Local Similarity 53.3%; Pred. No. 14;
 Matches 8; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 DWIWNQMHIDEEKN 15
 Db 39 DWIWSQ---EQEKEE 50

RESULT 13

Q8RYF1 PRELIMINARY; PRT; 176 AA.
 AC 08RYF1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative resistance protein (Fragment).
 GN RGA.
 OS *Avena striigosa* (black oat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Aveneae; *Avena*.
 OX NCBI_TaxId=38783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loarce Y., Iritoyen M.L., Fominaya A., Ferrer E.;
 RT "Resistance gene analogous in *Avena striigosa*.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ437574; CAD26862.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00931; NB-ARC; 1.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 176 AA; 20133 MW; D60982A15C6FE2FE CRC64;

Query Match 48.9%; Score 45; DB 10; Length 176;
 Best Local Similarity 58.3%; Pred. No. 21;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 TWNQMHIDEEKN 14
 Db 62 TWKSMNIDEEKD 73

RESULT 14

Q86T58

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ID Q86TS8 PRELIMINARY; PRT; 241 AA.
AC Q86TS8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Human full-length cDNA 5'-PRIME end of clone CSDB010YVP19 of placenta
DE of Homo sapiens (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RM [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Li W.B., Gruber C., Jessee J., Polayes D.,
RT "Full-length cDNA libraries and normalization."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RM EMBL: BX248750; CAD6557.1; -.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR Pfam: PF00028; cadherin. 2.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 2.
DR PROSITE: PS00232; CADHERIN_1; 1.
DR PROSITE: PS50268; CADHERIN_2; 2.
DR Plasmid.
KW NON TER
FT SEQUENCE 241 AA; 26348 MW; 4649831B55424604 CRC64;
SQ
Query Match 48.9%; Score 45; DB 4; Length 241;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 WINNQHIDE 12
Db 46 WINNQEYIER 56
RESULT 15
Q8IK72 PRELIMINARY; PRT; 241 AA.
AC Q8IK72;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein.
DE PF14_0734.
GN Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA Mefraden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter U.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum."

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RL Nature 419:498-511 (2002).
DR EMBL: AE014828; AAN37347.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF00069; kinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR Hypothetical protein.
KW SEQUENCE 241 AA; 28945 MW; 03664AF8F322F246 CRC64;
SQ
Query Match 48.9%; Score 45; DB 5; Length 241;
Best Local Similarity 44.4%; Pred. No. 29;
Matches 8; Conservative 3; Mismatches 3; Indels 4; Gaps 1;
QY 2 WINNQHIDE---DEKNE 15
Db 146 WINNQHILMDCSDPSKDE 163
Search completed: July 29, 2004, 11:37:09
Job time : 32 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:31:25 ; Search time 10.333 Seconds

(Without alignments)
139.633 Million cell updates/sec

Title: US-10-040-128-2

Sequence: 1 DWIMNQMHIDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	87	94.6	784	1 IJHUC5	cadherin 5 precursor - human
2	50	52.3	524	2 T20872	hypothetical prote
3	49	53.3	388	1 D38992	cadherin 8 - human
4	47.5	51.6	393	1 D70006	conserved hypothet
5	45	48.9	391	2 C69673	penicillin-binding
6	45	48.9	796	2 A38992	cadherin 11 precursor
7	45	48.9	796	2 I48277	cadherin-11 - mouse
8	45	48.9	796	2 I48556	cadherin-11 - mouse
9	45	48.9	796	2 A53584	OB-cadherin precursor
10	44.5	48.4	963	2 T09911	probable serine/thr
11	44	47.8	163	2 F89999	conserved hypothet
12	44	47.8	558	2 T29503	hypothetical prote
13	44	47.8	785	2 I50180	serine C-palmityl
14	44	47.8	790	2 I51638	cadherin-7 - chick
15	44	47.8	790	2 I51638	F-cadherin - Affric
16	44	47.8	790	2 I51638	cadherin-14 - huma
17	44	47.8	794	2 I59372	cadherin 12 - huma
18	43	46.7	435	2 C84941	histidinol dehydro
19	42	45.7	77	2 A11306	hypothetical prote
20	42	45.7	82	2 T46510	hypothetical prote
21	42	45.7	296	2 F95380	probable hydrolase
22	42	45.7	315	2 AG3535	dipeptide transpor
23	42	45.7	427	2 AF0590	citrate synthase [
24	41	44.6	77	2 A11678	hypothetical prote
25	41	44.6	314	2 S47696	nickel transport s
26	41	44.6	314	2 H91171	transport of nickel
27	41	44.6	314	2 H86017	transport of nickel
28	41	44.6	431	2 B82119	citrate synthase V
29	41	44.6	519	2 T33616	hypothetical prote

30	41	44.6	532	2 G90607	hypothetical prote
31	41	44.6	712	2 T16338	hypothetical prote
32	41	44.6	789	2 I52701	K-cadherin - rat
33	41	44.6	790	2 I37016	cadherin-6 - human
34	41	44.6	790	2 I50178	cadherin-6B - chic
35	41	44.6	2241	2 T20971	hypothetical prote
36	41	44.6	2261	2 T20978	hypothetical prote
37	41	44.6	6831	2 A88852	protein unc-22 (lim
38	41	44.6	6839	2 S57242	twlchlin (limlilari
39	41	44.6	7160	2 T27935	hypothetical prote
40	40.5	44.0	479	2 T23643	hypothetical prote
41	40	43.5	120	2 C72425	hypothetical prote
42	40	43.5	308	2 AB1957	hypothetical prote
43	40	43.5	308	2 G75264	hypothetical prote
44	40	43.5	355	2 T06122	probable lipase -
45	40	43.5	373	2 S48496	cysteine proteinas
					saccharopine dehyd

ALIGNMENTS

RESULT 1

IJHUC5

cadherin 5 precursor - human

N/Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #ext_change 22-Jun-1999

C/Accession: S49893; S24305; A43418

R/Breviario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp

submitted to the EMBL Data Library, June 1994

A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov

A/Reference number: S49893

A/Accession: S49893

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-784

A/Cross-References: EMBL:X59796; NID:G599833; PIDN:CA56306.1; PID:G599834

R/Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: S24305

A/Molecule type: mRNA

A/Residues: 5-516, 'I', 518-784 <SUZ>

A/Cross-References: EMBL:X59796; NID:G639976; PIDN:CA42468.1; PID:G29593

R/Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisecane, A.; Hosen, G.; Ruco,

J. Cell Biol. 118, 1511-1522, 1992

A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts

A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418

A/Molecule type: protein

A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-

A/Experimental source: cultured endothelial cells

A/Note: sequence extracted from NCBI backbone (NCBIF:113040, NCBIF:113045, NCBIF:113047,

C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t

C/Genetics:

A/Gene: GDB:CDH5

A/Cross-References: GDB:134230; OMIM:601120

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-47/Domain: propeptide #status predicted <PRO>

F:48-784/Product: cadherin 5 #status predicted <MAT>

F:48-593/Domain: extracellular #status predicted <EXT>

F:50-151/Domain: cadherin repeat homology <CR1>

F:154-258/Domain: cadherin repeat homology <CR2>

F:261-372/Domain: cadherin repeat homology <CR3>

F:375-479/Domain: cadherin repeat homology <CR4>

F:481-587/Domain: cadherin repeat homology <CR5>

F:594-620/Domain: transmembrane #status predicted <TM>

F:621-784/Domain: intracellular #status predicted <INT>

F:736-753/Region: serine-rich

F:61,112,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.6%; Score 87; DB 1; Length 784;

Best Local Similarity 100.0%; Pred. No. 7,6e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDEKN 14
|||||
DB 48 DWIMQMHIDEKN 61

RESULT 2

T20872
hypothetical protein F26H9.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C/Accession: T20872; T21443

R/Sims, M.
submitted to the EMBL Data Library, June 1996

A/Reference number: Z19337

A/Accession: T20872

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-524 <W1L>
A/Cross-references: EMBL:Z75535; PIDN:CAA9829.1; GSPDB:GN00019; CESP:F26H9.1

A/Experimental source: clone F14B4

R/Baynes, C.
submitted to the EMBL Data Library, November 1996

A/Reference number: Z19422

A/Accession: T21443

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-524 <W12>
A/Cross-references: EMBL:Z81516; PIDN:CAB04206.1; GSPDB:GN00019; CESP:F26H9.1

A/Experimental source: clone F26H9

C/Genetics:

A/Gene: CESP:F26H9.1

A/Map position: 1

A/Introns: 49/2; 99/1; 136/1; 186/1; 228/3; 287/3; 346/1; 403/1; 449/3

QY 2 WIMQMHIDEKN 15
|||
DB 486 WDMQNRNIDEHKNQ 499

RESULT 3

D38992
cadherin 8 - human

C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C/Accession: D38992

R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous

A/Reference number: S24305; WUID:91283540; PMID:2059658

A/Accession: D38992

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-793 <SUZ>
A/Cross-references: GB:L34060; NID:G506411; PIDN:AAA55628.1; PID:G506412

C/Genetics:

A/Gene: GDB:CDH8
A/cross-references: GDB:5822911
C/superfamily: cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication

F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 53.3%; Score 49; DB 2; Length 793;
Best Local Similarity 63.6%; Pred. No. 8.7;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WIMQMHIDE 12
|||
DB 56 WIMQMHIDE 66

RESULT 4

D70006
conserved hypothetical protein yuba - Bacillus subtilis

C/Species: Bacillus subtilis
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C/Accession: D70006

R/Kunst, F.; Ogatawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritzt, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogatawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segnuchi, J.; Sekowska, A.; Seror,

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpete, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; WUID:98044033; PMID:9384377

A/Accession: D70006

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-388 <KUN>

A/Cross-references: GB:Z99119; GB:AL009126; NID:G2635411; PIDN:CAB15094.1; PID:G2635600

A/Experimental source: strain 168

C/Genetics:

A/Gene: yuba

C/superfamily: Bacillus subtilis conserved hypothetical protein yuef

Query Match 51.6%; Score 47.5; DB 1; Length 388;

Best Local Similarity 62.5%; Pred. No. 6.8;

Matches 10; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 DWIMQMHIDEKN 15
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DB 366 DWFKWQSHLYDEKN 381

RESULT 5

C69673
penicillin-binding protein pbpx - Bacillus subtilis

C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C/Accession: C69673

R/Kunst, F.; Ogatawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritzt, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogatawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segnuchi, J.; Sekowska, A.; Seror,

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpete, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; WUID:98044033; PMID:9384377

A/Accession: C69673

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A;Residues: 1-391 <KUN>
 A;Cross-references: GB:299112; GB:AL009126; NID:G2633902; PIDN:CAB13568.1; PID:e1185286;
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: pdpX

Query Match 48.9%; Score 45; DB 2; Length 391;
 Best Local Similarity 53.8%; Pred. No. 17;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 3 WNMNMHIDEKNE 15
 Db 36 WNMALHNSSENE 48

RESULT 6
 A38992
 cadherin-11 precursor - human
 N;Alternate names: OB-cadherin, osteoblast
 C;Species: Homo sapiens (man)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
 C;Accession: A38992
 R;Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A;Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
 A;Reference number: S24305; MUID:91283540; PMID:2059658
 A;Accession: A38992
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-796 <SUZ>
 A;Cross-references: GB:134056; NID:G506403; PIDN:AAA35622.1; PID:G506404
 C;Genetics:
 A;Gene: GDB:CDH11; OB
 A;Cross-references: GDB:512891; OMIM:600023
 A;Map position: 16q22.1-16q22.1
 C;Superfamily: cadherin; cadherin repeat homology
 C;Keywords: calcium binding; cell adhesion; duplication
 F;56-159/Domain: cadherin repeat homology <CR1>
 F;162-268/Domain: cadherin repeat homology <CR2>
 F;271-383/Domain: cadherin repeat homology <CR3>
 F;386-488/Domain: cadherin repeat homology <CR4>

Query Match 48.9%; Score 45; DB 2; Length 796;
 Best Local Similarity 54.5%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNMNMHIDE 12
 Db 55 WNMNPFVIEE 65

RESULT 7
 148277
 cadherin-11 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C;Accession: 148277
 R;Hoffmann, I.; Balling, R.
 Dev. Biol. 169, 337-346, 1995
 A;Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
 A;Reference number: 148277; MUID:95269886; PMID:7750649
 A;Accession: 148277
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-796 <RES>
 A;Cross-references: EMBL:X77557; NID:G642796; PIDN:CAA54674.1; PID:G666071
 C;Genetics:
 A;Gene: cad-11
 C;Superfamily: cadherin; cadherin repeat homology
 F;56-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 45; DB 2; Length 796;
 Best Local Similarity 54.5%; Pred. No. 38;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 WNMNMHIDE 12
 Db 55 WNMNPFVIEE 65

RESULT 8
 149556
 cadherin-11 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C;Accession: 149556
 R;Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
 Dev. Biol. 169, 347-358, 1995
 A;Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
 A;Reference number: 149556; MUID:95269887; PMID:7750650
 A;Accession: 149556
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-796 <RES>
 A;Cross-references: GB:D31963; NID:G974190; PIDN:BA06730.1; PID:G974191
 F;56-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 45; DB 2; Length 796;
 Best Local Similarity 54.5%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNMNMHIDE 12
 Db 55 WNMNPFVIEE 65

RESULT 9
 A53584
 OB-cadherin precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
 C;Accession: A53584
 R;Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amann, E.
 J. Biol. Chem. 269, 12092-12098, 1994
 A;Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
 A;Reference number: A53584; MUID:94216322; PMID:816313
 A;Accession: A53584
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-796 <OKA>
 A;Cross-references: GB:D21253; NID:G994774; PIDN:BA04797.1; PID:G994775
 C;Superfamily: cadherin; cadherin repeat homology
 C;Keywords: transmembrane protein
 F;56-159/Domain: cadherin repeat homology <CR1>
 F;162-268/Domain: cadherin repeat homology <CR2>
 F;386-488/Domain: cadherin repeat homology <CR4>

Query Match 48.9%; Score 45; DB 2; Length 796;
 Best Local Similarity 54.5%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNMNMHIDE 12
 Db 55 WNMNPFVIEE 65

RESULT 10
 T09911
 Probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis th
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C;Accession: T09911
 R;Bevan, M.; Zimmermann, W.; Grunisen, A.; Wandut, R.; Bancroft, I.; Mewes, H.W.; Maye
 submitted to the Protein Sequence Database, June 1999
 A;Reference number: Z16896

A;Accession: T09911
 A;Molecule type: DNA
 A;Residues: 1-963 <BEV>
 A;Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.310
 A;Experimental source: cultivar Columbia; BAC clone T22A6
 C;Genetics:
 A;Gene: ATSP:T22A6.310
 A;Map position: 4
 A;Intons: 286/3; 386/2; 434/3; 473/2; 543/1; 678/1; 691/3; 719/3; 753/2; 788/3; 821/3;
 C;Keywords: phosphotransferase; protein kinase

Query Match 48.4%; Score 44.5; DB 2; Length 963;
 Best Local Similarity 50.0%; Pred. No. 56;
 Matches 7; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 DWI--NNQMHIDE 11
 ||: ||: ||:
 Db 660 DWLEVSNNELHIKE 673

RESULT 11
 F89999 conserved hypothetical protein SA1876 [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: F89999
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mutant-01, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: F89999
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-163 <KUR>
 A;Cross-references: GB:BA000018; PID:g13701867; PIDN:BA843159.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA1876

Query Match 47.8%; Score 44; DB 2; Length 163;
 Best Local Similarity 42.9%; Pred. No. 9.5;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 WIMNQHIDEKNE 15
 ||: ||: ||:
 Db 149 WIMNERHLENNKNE 162

RESULT 12
 B89962 hypothetical protein [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: B89962
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mutant-01, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: B89962
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-500 <KUR>
 A;Cross-references: GB:BA000018; PID:g13701565; PIDN:BA842858.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA1590

Query Match 47.8%; Score 44; DB 2; Length 500;
 Best Local Similarity 41.7%; Pred. No. 33;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DWIMQHIDE 12
 ||: ||: ||:
 Db 318 DWIMSLIEDQ 329

RESULT 13
 T29503 serine C-palmitoyltransferase (EC 2.3.1.50) F43H9.2 [similarity] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C;Accession: T29503
 R;Mu, X.; Le, T.
 submitted to the EMBL Data Library, February 1996
 A;Description: The sequence of C. elegans cosmid F43H9.
 A;Reference number: Z20629
 A;Accession: T29503
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-558 <WUX>
 A;Cross-references: EMBL:U50307; PIDN:AAA92303.1; CESP:F43H9.2
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CESP:F43H9.2
 A;Intons: 16/2; 71/3; 115/3; 289/1; 528/3
 C;Superfamily: serine C-palmitoyltransferase chain LCB2; glycine C-acetyltransferase hom
 C;Keywords: acyltransferase; coenzyme A; phosphoprotein; pyridoxal phosphate
 F;178-531/Domains: glycine C-acetyltransferase homology <GCA>
 F;184/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 47.8%; Score 44; DB 2; Length 558;
 Best Local Similarity 58.3%; Pred. No. 37;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNOEHDEKNE 15
 ||: ||: ||:
 Db 29 WNOEHDEDEE 40

RESULT 14
 IS0180 cadherin-7 - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C;Accession: IS0180
 R;Nakagawa, S.; Takeichi, M.
 Development 121, 1321-1332, 1995
 A;Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-spec
 A;Reference number: IS0178; MUID:95309115; PMID:7540531
 A;Accession: IS0180
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-785 <NAK>
 A;Cross-references: GB:DA2150; NID:9868000; PIDN:BA00721.1; PID:9868001
 C;Superfamily: cadherin; cadherin repeat homology
 F;156-262/Domains: cadherin repeat homology <CH>

Query Match 47.8%; Score 44; DB 2; Length 785;
 Best Local Similarity 54.5%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WIMNQHIDE 12
 ||: ||: ||:
 Db 49 WVMNQFFVLEE 59

RESULT 15
 IS1638 F-cadherin - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
 C;Accession: IS1638; SS5391

R;Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A;Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A;Reference number: 151638; MUID:96039533; PMID:7496627
A;Accession: 151638
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-790 <ESP>
A;Cross-references: EMBL:X85330; NID:9854634; PIDD:CAA59679.1; PID:9854635
C;Superfamily: cadherin; cadherin repeat homology
F;161-267/Domain: cadherin repeat homology <CR2>

Query Match 47.8%; Score 44; DB 2; Length 790;
Best Local Similarity 54.5%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WINQMHIDE 12
|:|:|:|:
Db 54 WVNQFFVLEE 64

Search completed: July 29, 2004, 11:37:50
Job time : 11.333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:29:40 ; Search time 46.6667 Seconds

(without alignments)
90.819 Million cell updates/sec

Title: US-10-040-128-2

Sequence: 1 DWMNQMHIDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq 290404:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	15	AAU08778	VE-cadher
2	92	100.0	103	AAU08786	Murine VE
3	87	94.6	15	AAU08779	VE-cadher
4	87	94.6	104	AAU08785	Human VE-
5	87	94.6	108	AAV64578	Nonclassi
6	87	94.6	566	AAU11276	Human rec
7	87	94.6	594	AAU11279	Human rec
8	87	94.6	780	AAW25634	Human rec
9	87	94.6	780	AAW13130	Human cad
10	87	94.6	784	ABR81477	Full leng
11	87	94.6	784	ABU03507	Human VE-
12	87	94.6	784	ABU03507	Angiogene
13	87	94.6	784	ADA03363	Lung canc
14	87	94.6	15	AAU08777	Human vas
15	52	56.5	167	ABO00590	VE-cadher
16	52	56.5	772	AAV41725	Novel hum
17	52	56.5	772	AAV41725	Human PRO
18	52	56.5	772	AAV41725	Human PRO
19	52	56.5	772	AAV41725	Human PRO
20	52	56.5	772	AAV41725	Human PRO
21	52	56.5	772	AAV41725	Human PRO
22	52	56.5	772	AAV41725	Human PRO
23	52	56.5	772	AAV41725	Human PRO
24	52	56.5	772	AAV41725	Human PRO
25	52	56.5	772	AAV41725	Human PRO

26	52	56.5	772	6	ABU82758	Human PRO
27	52	56.5	772	6	ABU89879	Novel hum
28	52	56.5	772	6	ABR68128	Human sec
29	52	56.5	772	6	ABU96181	Novel hum
30	52	56.5	772	6	ABU92612	Human sec
31	52	56.5	772	6	ABO08689	Human sec
32	52	56.5	772	6	ABO02741	Human sec
33	52	56.5	772	6	ABR74895	Human sec
34	52	56.5	772	6	ABR94657	Human sec
35	52	56.5	772	6	ABO25180	Novel hum
36	52	56.5	772	6	ABO25227	Novel hum
37	52	56.5	772	6	ABU85630	Human PRO
38	52	56.5	772	6	ABU98790	Human PRO
39	52	56.5	772	6	ABU98005	Novel hum
40	52	56.5	772	6	ABU91711	Novel hum
41	52	56.5	772	6	ABU72233	Novel hum
42	52	56.5	772	6	ABU89404	Human PRO
43	52	56.5	772	6	ABU86245	Human sec
44	52	56.5	772	6	ABU67458	Human sec
45	52	56.5	772	6	ABU80486	Human PRO

ALIGNMENTS

RESULT 1	AAU08778	standard; peptide; 15 AA.
ID	AAU08778	
XX	AAU08778	
AC	AAU08778	
DT	27-FEB-2002	(first entry)
DE	VE-cadherin N-terminal domain 1 antibody binding peptide #2.	
XX	VE-cadherin N-terminal domain 1 antibody binding peptide #2.	
KW	VE-cadherin; antibody binding peptide; angiogenesis; neoplastic disease;	
KW	VE-cadherin mediated adherens junction formation; autoimmune disease;	
KW	paracellular permeability; solid tumour; collagenous vascular disease;	
KW	rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;	
KW	retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;	
KW	carcinoma; sarcoma; adenocarcinoma; adenoma; gene therapy;	
KW	leukaemic tumour; lymphoid tumours; cell proliferation disorder;	
KW	vasculatization; blood vessel proliferation disorder; fibrotic disorder;	
KW	age-related muscular degeneration; tumour neovascularization;	
KW	VE-cadherin N-terminal domain 1.	
OS	Mammalia.	
XX	WO200175109-A2.	
PN	11-OCT-2001.	
XX	30-MAR-2001; 2001WO-US010505.	
PD	31-MAR-2000; 2000US-00540967.	
PF	(IMCL-) IMCLONE SYSTEMS INC.	
XX	Liao F, Hicklin DJ, Bohlen P;	
XX	WPI; 2001-6556986/75.	
DR	New antibody antagonists of VE-cadherin, which does not adversely affect	
PT	vascular permeability, useful for inhibiting angiogenesis or tumor	
PT	metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.	
XX	Claim 1; Page 32; 44pp; English.	
XX	The method relates to an antibody or an antibody fragment, capable of	
CC	specifically binding to a VE-cadherin, and of inhibiting VE-cadherin	
CC	mediated adherens junction formation in vitro, but does not exert any	
CC	significant or substantial effect on paracellular permeability in vitro.	
CC	The antibody or antibody fragment is capable of specifically binding to a	

```
CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
CC disease, a solid tumour, an autoimmune disease, collagenous vascular
CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas, The
CC adenocarcinomas, adenomas, leukaemic tumours or lymphoid tumours). The
CC composition or antibody is also useful for treating a cell proliferation
CC disorder associated with vascularisation (e.g. blood vessel proliferation
CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
CC These may also be used for reducing or inhibiting tumour vasculature in a
CC mammal. The nucleic acid that encodes the antibody or is useful in gene
CC therapy, particularly for inhibiting angiogenesis or tumour
CC neovascularisation. This sequence represents a VE-cadherin N-terminal
CC domain 1 antibody binding peptide
CC
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 92; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DWINQMHIDEKKE 15
DB 1 DWINQMHIDEKKE 15
| | | | | | | | | | | | | | |
AAU08786;
27-FEB-2002 (first entry)
MURINE VE-CADHERIN N-TERMINAL DOMAIN 1 POLYPEPTIDE.
DE
XX VE-cadherin; angiogenesis; neoplastic disease;
XX VE-cadherin mediated adherens junction formation; autoimmune disease;
XX paracellular permeability; solid tumour; collagenous vascular disease;
XX rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
XX retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
XX carcinoma; sarcoma; adenocarcinoma; adenomas; gene therapy;
XX leukaemic tumour; lymphoid tumours; cell proliferation disorder;
XX vascularisation; blood vessel proliferation disorder; fibrotic disorder;
XX age-related muscular degeneration; tumour neovascularisation; mouse;
XX VE-cadherin N-terminal domain 1.
XX
OS Mus sp.
XX
XX WO200175109-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010505.
XX
XX 31-MAR-2000; 2000US-00540967.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Liao F, Hicklin DJ, Bohlen P;
XX
XX WPI; 2001-656988/75.
XX
XX
XX New antibody antagonists of VE-cadherin, which does not adversely affect
XX vascular permeability, useful for inhibiting angiogenesis or tumour
XX metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.
XX
XX Example 2; Fig 2; 44pp; English.
XX
XX The method relates to an antibody or an antibody fragment, capable of
```

```
CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
CC mediated adherens junction formation in vitro, but does not exert any
CC significant or substantial effect on paracellular permeability in vitro.
CC The antibody or antibody fragment is capable of specifically binding to a
CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
CC disease, a solid tumour, an autoimmune disease, collagenous vascular
CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas, The
CC adenocarcinomas, adenomas, leukaemic tumours or lymphoid tumours). The
CC composition or antibody is also useful for treating a cell proliferation
CC disorder associated with vascularisation (e.g. blood vessel proliferation
CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
CC These may also be used for reducing or inhibiting tumour vasculature in a
CC mammal. The nucleic acid that encodes the antibody or is useful in gene
CC therapy, particularly for inhibiting angiogenesis or tumour
CC neovascularisation. This sequence represents a murine VE-cadherin N-
CC terminal domain 1 polypeptide
CC
XX
SQ Sequence 103 AA;
Query Match 100.0%; Score 92; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DWINQMHIDEKKE 15
DB 1 DWINQMHIDEKKE 15
| | | | | | | | | | | | | | |
AAU08779;
27-FEB-2002 (first entry)
MURINE VE-CADHERIN N-TERMINAL DOMAIN 1 ANTIBODY BINDING PEPTIDE #3.
DE
XX VE-cadherin N-terminal domain 1 antibody binding peptide #3.
XX
XX VE-cadherin; antibody binding peptide; angiogenesis; neoplastic disease;
XX VE-cadherin mediated adherens junction formation; autoimmune disease;
XX paracellular permeability; solid tumour; collagenous vascular disease;
XX rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
XX retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
XX carcinoma; sarcoma; adenocarcinoma; adenomas; gene therapy;
XX leukaemic tumour; lymphoid tumours; cell proliferation disorder;
XX vascularisation; blood vessel proliferation disorder; fibrotic disorder;
XX age-related muscular degeneration; tumour neovascularisation;
XX VE-cadherin N-terminal domain 1.
XX
XX Mammalia.
XX
XX WO200175109-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010505.
XX
XX 31-MAR-2000; 2000US-00540967.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Liao F, Hicklin DJ, Bohlen P;
XX
XX WPI; 2001-656988/75.
XX
XX
XX New antibody antagonists of VE-cadherin, which does not adversely affect
XX vascular permeability, useful for inhibiting angiogenesis or tumour
XX metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.
XX
XX
```

XX Claim 1; Page 32; 44pp; English.
 PS
 XX The method relates to an antibody or an antibody fragment, capable of
 CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
 CC mediated adherens junction formation in vitro, but does not exert any
 CC significant or substantial effect on paracellular permeability in vitro.
 CC The antibody or antibody fragment is capable of specifically binding to a
 CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
 CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
 CC angiogenesis (e.g. angiogenesis in an autoimmune disease, collagenous vascular
 CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
 CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
 CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas,
 CC adenosarcomas, adenomas, leukaemic tumours or lymphoid tumours). The
 CC composition or antibody is also useful for treating a cell proliferation
 CC disorder associated with vascularisation (e.g. blood vessel proliferation
 CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
 CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
 CC These may also be used for reducing or inhibiting tumour vasculature in a
 CC mammal. The nucleic acid that encodes the antibody or is useful in gene
 CC therapy, particularly for inhibiting angiogenesis or tumour
 CC neovascularisation. This sequence represents a VE-cadherin N-terminal
 CC domain 1 antibody binding peptide
 XX
 SQ Sequence 15 AA;
 Query Match 94.6%; Score 87; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DWIMQMHIDEKN 14
 Db 1 DWIMQMHIDEKN 14
 RESULT 4
 AAU08785
 ID AAU08785 standard; protein; 104 AA.
 XX
 AC AAU08785;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human VE-cadherin N-terminal domain 1 polypeptide.
 XX
 KW VE-cadherin; angiogenesis; neoplastic disease;
 KW paracelluar mediated adherens junction formation; autoimmune disease;
 KW paracelluar permeability; solid tumour; collagenous vascular disease;
 KW rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
 KW retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
 KW leiomyoma; sarcoma; adenocarcinoma; adenosarcoma; adenoma; gene therapy;
 KW leukaemic tumour; lymphoid tumours; cell proliferation disorder;
 KW vascularisation; blood vessel proliferation disorder; fibrotic disorder;
 KW age-related muscular degeneration; tumour neovascularisation; human;
 KW VE-cadherin N-terminal domain 1.
 XX
 OS Homo sapiens.
 XX
 PN WO200175109-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US010505.
 XX
 PR 31-MAR-2000; 2000US-00540967.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Liao F, Hicklin DJ, Bohlen P;
 XX
 DR WPI, 2001-656988/75.

XX New antibody antagonists of VE-cadherin, which does not adversely affect
 PT vascular permeability, useful for inhibiting angiogenesis or tumor
 PT metastasis, e.g. autoimmune disease, carcinomas or leukaemic tumors.
 XX
 PS Example 2; Fig 2; 44pp; English.
 XX
 CC The method relates to an antibody or an antibody fragment, capable of
 CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
 CC mediated adherens junction formation in vitro, but does not exert any
 CC significant or substantial effect on paracellular permeability in vitro.
 CC The antibody or antibody fragment is capable of specifically binding to a
 CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
 CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
 CC angiogenesis (e.g. angiogenesis in an autoimmune disease, collagenous vascular
 CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
 CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
 CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas,
 CC adenosarcomas, adenomas, leukaemic tumours or lymphoid tumours). The
 CC composition or antibody is also useful for treating a cell proliferation
 CC disorder associated with vascularisation (e.g. blood vessel proliferation
 CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
 CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
 CC These may also be used for reducing or inhibiting tumour vasculature in a
 CC mammal. The nucleic acid that encodes the antibody or is useful in gene
 CC therapy, particularly for inhibiting angiogenesis or tumour
 CC neovascularisation. This sequence represents a human VE-cadherin N-
 CC terminal domain 1 polypeptide
 XX
 SQ Sequence 104 AA;
 Query Match 94.6%; Score 87; DB 4; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DWIMQMHIDEKN 14
 Db 1 DWIMQMHIDEKN 14
 RESULT 5
 AAY64578
 ID AAY64578 standard; peptide; 108 AA.
 XX
 AC AAY64578;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Nonclassical cadherin extracellular domain SEQ ID NO:6.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease.
 XX
 OS Mammalia.
 XX
 PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 XX
 PR 06-NOV-1998; 98US-00187859.
 XX
 PR 20-JAN-1999; 99US-00234395.
 XX
 PR 08-MAR-1999; 99US-00264516.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Gour BJ, Byers S;
 PI MPI; 2000-038791/03.
 XX
 DR
 PT New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Disclosure; Fig 2; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA23183 to AA23186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 108 AA;
 Query Match 94.6%; Score 87; DB 3; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DWIMNQMHIIDEKN 14
 Db 5 DWIMNQMHIIDEKN 18
 RESULT 6
 ID AAU11276 standard; protein; 566 AA.
 AC AAU11276;
 DT 26-MAR-2002 (first entry)
 XX
 DE Human recombinant KVE702 polypeptide.
 XX
 KM Human; KV protein; KVE702; angiogenic factor antagonist; angiogenesis;
 KM vascular endothelial structure regulator; cancer; vascular endothelium;
 KM tumour; blood vessel; epithelial cell; cytosstatic; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200183562-A2.
 PD 08-NOV-2001.
 PF 04-MAY-2001; 2001WO-GB001956.
 PR 04-MAY-2000; 2000GB-00010630.
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

XX
 PI Jiang WG;
 XX
 DR MPI; 2002-066521/09.
 DR N-PSDB; AAS16965.
 XX
 PT Novel nucleic acid for inhibition of angiogenesis and prophylaxis or
 PT treatment of cancer, comprises both an angiogenic factor antagonist and a
 PT vascular endothelial structure regulator.
 XX
 PS Disclosure; Fig 2; 66pp; English.
 XX
 CC The invention relates to recombinant nucleic acid sequences that encode
 CC both an angiogenic factor antagonist and a vascular endothelial structure
 CC regulator, collectively referred to as a KV protein. KV DNA and proteins,
 CC and also cells and compositions containing the sequences, are useful in
 CC treating or preventing cancer or angiogenesis in mammals, in particular
 CC humans. KV proteins are also useful for regulation of the development of
 CC blood vessels and their formation, in the vascular endothelium and/or
 CC tumour. The KVE702 gene and its fragments are useful in transfection of
 CC human epithelial cells and to generate products suitable for angiogenesis
 CC intervention. This sequence represents the human KVE702 protein
 XX
 SQ Sequence 566 AA;
 Query Match 94.6%; Score 87; DB 5; Length 566;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DWIMNQMHIIDEKN 14
 Db 474 DWIMNQMHIIDEKN 487
 RESULT 7
 ID AAU11279 standard; protein; 594 AA.
 AC AAU11279;
 DT 26-MAR-2002 (first entry)
 XX
 DE Human recombinant U37 polypeptide.
 XX
 KM Human; KV protein; KVE702; angiogenic factor antagonist; angiogenesis;
 KM vascular endothelial structure regulator; cancer; vascular endothelium;
 KM tumour; blood vessel; epithelial cell; cytosstatic; gene therapy; U37.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200183562-A2.
 PD 08-NOV-2001.
 PF 04-MAY-2001; 2001WO-GB001956.
 PR 04-MAY-2000; 2000GB-00010630.
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 PI Jiang WG;
 XX
 DR MPI; 2002-066521/09.
 DR N-PSDB; AAS16975.
 XX
 PT Novel nucleic acid for inhibition of angiogenesis and prophylaxis or
 PT treatment of cancer, comprises both an angiogenic factor antagonist and a
 PT vascular endothelial structure regulator.

XX PS Disclosure; Fig 15; 66pp; English.
 XX CC
 CC The invention relates to recombinant nucleic acid sequences that encode
 CC both an angiogenic factor antagonist and a vascular endothelial structure
 CC regulator, collectively referred to as a KV protein. KV DNA and proteins,
 CC and also cells and compositions containing the sequences, are useful in
 CC treating or preventing cancer or angiogenesis in mammals, in particular
 CC humans. KV proteins are also useful for regulation of the development of
 CC blood vessels and their formation, in the vascular endothelium and/or
 CC tumour. The KVE702 gene and its fragments are useful in transfection of
 CC human epithelial cells and to generate products suitable for angiogenesis
 CC intervention. This sequence represents the human J37 protein used in
 CC methods of the invention
 XX SQ Sequence 594 AA;
 XX
 XX Query Match 94.6%; Score 87; DB 5; Length 594;
 XX Best Local Similarity 100.0%; Pred. No. 7.1e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 DW1WQMHIDEKN 14
 XX |||||
 XX 49 DW1WQMHIDEKN 62
 XX Db
 XX
 XX RESULT 8
 XX AAW25634
 XX ID AAW25634 standard; protein; 780 AA.
 XX AC AAW25634;
 XX XX
 XX DT 25-MAR-2003 (revised)
 XX DT 03-NOV-1997 (first entry)
 XX DE Human cadherin-5.
 XX KW Human; cadherin; rat; calcium-dependent cell adhesion protein;
 XX KM superfamily; cytoskeleton; eatenin; cancer.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 XX FT Misc-difference 622
 XX FT note="encoded by AAG"
 XX XX
 XX PN US5646250-A.
 XX PD 08-JUL-1997.
 XX PF 01-NOV-1994; 94US-00332638.
 XX PR 17-APR-1992; 92US-00872643.
 XX PR 19-APR-1993; 93US-00049460.
 XX PA (DOHE-) DOHENY EYE INST.
 XX PI Suzuki S;
 XX DR WPI; 1997-362997/33.
 XX DR N-PSDB; AAT85401.
 XX PT Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion.
 XX PS Claim 1; Col 69-72; 56pp; English.
 XX CC This sequence represents human cadherin-5. The invention specifically
 CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat
 CC cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell
 CC adhesion proteins. They are glycosylated integral membrane proteins that
 CC have an N-terminal extracellular domain that determines binding
 CC specificity, a hydrophobic membrane spanning region and a C-terminal
 CC cytoplasmic domain, which is highly conserved among members of the

CC superfamily. The C-terminal domain interacts with the cytoskeleton
 CC through eatenins and other cytoskeleton-associated proteins. The novel
 CC cadherin proteins may be used in the analysis of the role of cadherins in
 CC various cancers. Sequence analysis of the cadherin proteins also allows
 CC investigation of the structure and function of cadherin. The cadherin
 CC proteins may be isolated by using anti-cadherin antibodies. These
 CC antibodies may also be used to modulate the activity of cadherin and to
 CC determine the tissue specific distribution of cadherin proteins. Each
 CC subclass of cadherins has a unique tissue distribution pattern. (updated
 CC on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 780 AA;
 XX
 XX Query Match 94.6%; Score 87; DB 2; Length 780;
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 DW1WQMHIDEKN 14
 XX |||||
 XX 44 DW1WQMHIDEKN 57
 XX Db
 XX
 XX RESULT 9
 XX AAW13130
 XX ID AAW13130 standard; protein; 780 AA.
 XX AC AAW13130;
 XX XX
 XX DT 25-MAR-2003 (revised)
 XX DT 13-MAY-1997 (first entry)
 XX DE Full length human cadherin-5.
 XX KW Ca2+ dependent; cell adhesion protein; placental; cadherin; rat; brain;
 XX KM human; antibody; purification; determination; tissue expression;
 XX binding antagonist; calcium ion.
 XX OS Homo sapiens.
 XX PH US5597725-A.
 XX PN 28-JAN-1997.
 XX PD 26-JAN-1994; 94US-00188228.
 XX PR 17-APR-1992; 92US-00872643.
 XX PR 19-APR-1993; 93US-00049460.
 XX PA (DOHE-) DOHENY EYE INST.
 XX PI Suzuki S;
 XX DR WPI; 1997-108328/10.
 XX DR N-PSDB; AAT61921.
 XX PT Antibodies to cadherin proteins - useful as cadherin antagonists, etc.
 XX PS Claim 5; Col 75-78; 59pp; English.
 XX CC The present sequence is full length human cadherin-5, which is a Ca2+
 CC dependent cell adhesion protein. The human cadherin cDNA was isolated
 CC from a placental cDNA library, using probes based on homologous rat
 CC cadherin cDNA. Antibodies or fragments that specifically bind the human
 CC cadherin can be used to purify the cadherin, determine its tissue
 CC expression and antagonise its ligand/antiligand binding activities.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 780 AA;
 XX
 XX Query Match 94.6%; Score 87; DB 2; Length 780;
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIWMQHIDEKN 14
 DB 44 DWIWMQHIDEKN 57

RESULT 10

ID ABB81477 standard; protein; 784 AA.

AC ABB81477;

DT 30-AUG-2002 (first entry)

DE Human VE-cadherin protein SEQ ID NO:52.

XX Cadherin; alpha-catenin; cancer; beta-catenin binding domain; melanoma;
 XX o-catenin; colon cancer.

OS Homo sapiens.

PN US2002045591-A1.

PD 18-APR-2002.

PF 17-JUL-2001; 2001US-00905983.

PR 26-MAY-1998; 98IL-00124650.

PR 26-MAY-1999; 99US-00318633.

PA (GEIGER/) GEIGER B.

PA (BERNZ/) BEN-ZE'EV A.

PA (SADOT/) SADOT E.

PI Geiger B, Ben-Ze'ev A, Sadot E;

XX WPI; 2002-499105/53.

DR N-PSDB; AEN89394.

PT New construct encoding soluble cytoplasmic portion of cadherin including
 PT beta catenin binding domain useful in treating cancer associated with
 PT high beta-catenin activity e.g. colon cancer and melanoma.

PS Example 3; Page 56-58; 102pp; English.

CC The present invention describes a pharmaceutical composition for treating
 CC cancer associated with abnormally high beta-catenin activity. The
 CC pharmaceutical composition comprises a gene therapy vehicle harbouring a
 CC polynucleotide that contains: (1) a nucleotide sequence encoding a
 CC soluble cytoplasmic portion of a cadherin which lacks a transmembrane
 CC portion and an extracellular portion of the cadherin, and includes a beta
 CC -catenin binding domain; and (b) an upstream promoter for directing
 CC expression of the soluble cytoplasmic portion of the cadherin in a
 CC mammalian cell. Also described is a pharmaceutical composition for
 CC treating cancer associated with abnormally high activity levels of beta-
 CC catenin comprising a gene therapy vehicle harbouring a polynucleotide
 CC that contains: (a) a nucleotide sequence encoding an o-catenin; and (b)
 CC an upstream promoter for directing expression of the o-catenin in a
 CC mammalian cell. The pharmaceutical compositions have cytostatic activity
 CC and can be used in the suppression of beta-catenin-mediated
 CC transactivation. They can be used for treating cancers associated with
 CC abnormally high activity levels of beta-catenin such as colon cancers and
 CC melanomas, by reducing these high activity levels of beta-catenin in
 CC mammalian cells. The present sequence represents human VE-cadherin which
 CC is used in the exemplification of the present invention

XX Sequence 784 AA;

QY Query Match 94.6%; Score 87; DB 5; Length 784;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DWIWMQHIDEKN 14
 |||

DB 48 DWIWMQHIDEKN 61

RESULT 11

ID ABU03507 standard; protein; 784 AA.

AC ABU03507;

DT 21-JAN-2003 (first entry)

DE Angiogenesis-associated human protein sequence #52.

XX Human; angiogenesis-associated transcript; angiogenesis;
 XX angiogenesis-associated disease; cancer; cytostatic.

OS Homo sapiens.

PN WO200279492-A2.

PD 10-OCT-2002.

PF 14-FEB-2002; 2002WO-US004915.

PR 14-FEB-2001; 2001US-00784356.

PR 22-FEB-2001; 2001US-00791390.

PR 19-APR-2001; 2001US-0285475P.

PR 03-AUG-2001; 2001US-0310025P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334244P.

PA (BOSB-) EOS BIOTECHNOLOGY INC.

PI Murray R, Glynn R, Watson SR, Aziz N;

XX WPI; 2003-040681/03.

DR N-PSDB; ABX08791.

PT Detecting angiogenesis-associated transcript in a cell for diagnosing and
 PT treating cancer by contacting a sample with a polynucleotide that
 PT exhibits changes in expression level as a function of time in tissue
 PT undergoing angiogenesis.

PS Example 2; Page 230; 291pp; English.

CC The present invention relates to methods and compositions for detecting
 CC an angiogenesis-associated transcript in a cell in a patient. The method
 CC involves contacting a biological sample from the patient with a
 CC polynucleotide that selectively hybridises to a sequence at least 80%
 CC identical to any of the angiogenesis-associated human polynucleotide
 CC sequences given in the specification. These angiogenesis-associated
 CC polynucleotide sequences comprise genes that exhibit changes in
 CC expression levels as a function of time in tissue undergoing
 CC angiogenesis. The method and the polynucleotide sequences of the
 CC invention are useful for diagnosing and treating angiogenesis and
 CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
 CC sequences are also useful in the gene therapy of such disorders. The
 CC angiogenesis-associated proteins encoded by the polynucleotide sequences
 CC are useful as a vaccine for therapeutic and prophylactic immunisation.
 CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences

XX Sequence 784 AA;

QY Query Match 94.6%; Score 87; DB 6; Length 784;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 DWIWMQHIDEKN 61

RESULT 12

ABU56570
ID ABU56570 standard; protein; 784 AA.
XX
AC ABU56570;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #163.
XX
KW Lung cancer-associated polypeptide; cyrostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
XX
PR 10-MAY-2001; 2001US-0290492P.
XX
PR 09-NOV-2001; 2001US-0339245P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 29-NOV-2001; 2001US-0334370P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI: 2003-093161/08.
XX
DR N-PSDB; ABX76299.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 314; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 784 AA;
XX
Query Match 94.6%; Score 87; DB 6; Length 784;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DWINQWHIDEKN 14
DB 48 DWINQWHIDEKN 61

RESULT 13
IDA03363
ID ADA03363 standard; protein; 784 AA.
XX
AC ADA03363;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human vascular endothelial cadherin protein.
XX
KW cyrostatic; antidiabetic; ophthalmological; antiarthritic;
KW endostatin receptor; angiogenesis inhibitor; human;
KW vascular endothelial cadherin; angiogenesis; blood vessel; cancer;
KW diabetic retinopathy; rheumatoid arthritis; receptor.
XX
OS Homo sapiens.
XX
PN WO2003038096-A1.
XX
PD 08-MAY-2003.
XX
PF 28-OCT-2002; 2002WO-JP011143.
XX
PR 30-OCT-2001; 2001JP-00333295.
XX
PA (KUBO/) KUBOTA S.
XX
PA (NEMO/) NEMOTO T.
XX
PI Kubota S, Nemoto T;
XX
DR WPI: 2003-430528/40.
XX
DR N-PSDB; ADA03362.
XX
PT Vascular endothelial cadherin is a receptor to endostatin for screening
PT endostatin agonists and antagonists as angiogenesis inhibitors and
PT remedies for cancer development and proliferation.
XX
PS Claim 2; Page 44-47; 56pp; Japanese.
XX
CC The invention relates to a DNA encoding an endostatin receptor protein
CC (human vascular endothelial (VE) cadherin (1)) or its partial peptides or
CC encoding a protein derived from (1) by addition, deletion or substitution
CC of one or more amino acid residues and having similar binding activity to
CC endostatin. The sequence can be used in the regulation of angiogenesis in
CC the treatment and prevention of diseases associated with the formation of
CC new blood vessels, including cancer, cancer proliferation, diabetic
CC retinopathy and rheumatoid arthritis. This sequence corresponds to the VE
CC cadherin protein which serves as an endostatin receptor protein.
XX
SQ Sequence 784 AA;
XX
Query Match 94.6%; Score 87; DB 6; Length 784;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DWINQWHIDEKN 14
DB 48 DWINQWHIDEKN 61
RESULT 14
AAU08777
ID AAU08777 standard; peptide; 15 AA.
XX
AC AAU08777;
XX
DT 27-FEB-2002 (first entry)
XX
DE VE-cadherin N-terminal domain 1 antibody binding peptide #1.
XX
KW VE-cadherin; antibody binding peptide; angiogenesis; neoplastic disease;

XX	VE-cadherin mediated adherens junction formation; autoimmune disease;
XX	paraneoplastic permeability; solid tumour; collagenous vascular disease;
XX	rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
XX	retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
KW	carcinoma; sarcoma; adenocarcinoma; adenosarcoma; adenoma; gene therapy;
KM	leukaemic tumour; lymphoid tumours; cell proliferation disorder;
KV	vascularisation; blood vessel proliferation disorder; fibrotic disorder;
KW	age-related muscular degeneration; tumour neovascularisation;
KX	VE-cadherin N-terminal domain 1.
OS	Mammalia.
PN	WO200175109-A2.
PP	11-OCT-2001.
XP	30-MAR-2001; 2001WO-US010505.
XX	31-MAR-2000; 2000US-00540967.
PR	(IMCL-) IMCLONE SYSTEMS INC.
PA	Liso F, Hicklin DJ, Bohlen P;
PI	WPI; 2001-656988/75.
DR	New antibody antagonists of VE-cadherin, which does not adversely affect
PT	vascular permeability, useful for inhibiting angiogenesis or tumor
PS	metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.
XX	Claim 1; Page 32; 44pp; English.
XX	The method relates to an antibody or an antibody fragment, capable of
CC	specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
CC	mediated adherens junction formation in vitro, but does not exert any
CC	significant or substantial effect on paracellular permeability in vitro.
CC	The antibody or antibody fragment is capable of specifically binding to a
CC	site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
CC	a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
CC	angiogenesis (e.g. angiogenesis that is associated with a neoplastic
CC	disease, a solid tumour, an autoimmune disease, collagenous vascular
CC	disease, rheumatoid arthritis, an ophthalmological condition, diabetic
CC	retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
CC	metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas,
CC	adenosarcomas, adenomas, leukaemic tumours or lymphoid tumours). The
CC	composition or antibody is also useful for treating a cell proliferation
CC	disorder associated with vascularisation (e.g. blood vessel proliferation
CC	disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
CC	metastasis, rheumatoid arthritis or age-related muscular degeneration).
CC	These may also be used for reducing or inhibiting tumour vasculature in a
CC	mammal. The nucleic acid that encodes the antibody or is useful in gene
CC	therapy, particularly for inhibiting angiogenesis or tumour
CC	neovascularisation. This sequence represents a VE-cadherin N-terminal
XX	domain 1 antibody binding peptide
SQ	Sequence 15 AA:
Query Match	84.8%; Score 78; DB 4; Length 15;
Best Local Similarity	93.3%; Pred. No. 2.8e-05;
Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 DWIWMQHIDEKNE 15 1 DELWMQHIDEKNE 15
RESULT 15	
AEOO00590	ID ABOO00590 standard; protein; 167 AA.
AC	ABO00590;
XX	06-AUG-2003 (first entry)
DT	

XX Novel human polypeptide #177.

XX Human: angiogenesis; cytokine; cell proliferation; pluripotent;
KW cell differentiation; totipotent; stem cell; transplantation; bio-sensor;
KW neuroepithelial cell; autoimmune disease; neural cell; genetic disorder;
KW nerve; brain tissue; central nervous system disease;
KW peripheral nervous system disease; neuropathy; haematopoiesis; bone;
KW myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;
KW regeneration; cartilage; tendon; ligament; nerve tissue growth;
KW tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;
KW osteoarthritis; bone degenerative disorder; periodontal disease;
KW gut protection; lung fibrosis; liver fibrosis; reperfusion injury;
KW immune deficiency; infection; autoimmune disorder; allergic reaction;
KW thrombolytic; thrombosis; coagulation disorder; hereditary disorder;
KW biochem; circadian cycle; fertility; metabolism; catabolism; anabolism;
KW neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
KW haemostatic; vulnery; antiulcer; osteopathic; antiarthritic;
KW vasostrophic; immunostimulant; antibacterial; fungicide; immunosuppressive;
KW antirheumatic; antidiabetic; antisthmatic; cyrostatic; virucide.

OS Homo sapiens.

XX WO2003023013-A2.

XX 20-MAR-2003.

XX 13-SEP-2002; 2002MO-US029001.

XX 13-SEP-2001; 2001US-0322511P.

XX 12-SEP-2002; 2002US-00243552.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Yang Y, Wang Z, Weng G, Ma Y;

PT WPI; 2003-313249/30.

DR N-PSDB; ACD05667.

XX Novel nucleic acids and polypeptides for diagnosis, treatment of central
PT and peripheral nervous system diseases and neuropathies, such as
PT Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
PT lateral sclerosis.

XX Claim 20; SEQ ID NO 513; 300bp; English.

XX The present invention relates to the isolation of novel human
CC polynucleotide sequences and their encoding polypeptides. The novel
CC polypeptides exhibit activities relating to angiogenesis, cytokine, cell
CC proliferation, cell differentiation, antiinflammatory, and stem cell
CC growth factor activities. The polypeptides are involved in the
CC proliferation, differentiation and survival of pluripotent and totipotent
CC stem cells, and are useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals and
CC development of bio-sensors. The polypeptides can be used to manipulate
CC stem cells in culture to give rise to neuroepithelial cells that can be
CC used to augment or replace cells damaged by illness, autoimmune disease,
CC accidental damage or genetic disorders. The polypeptides induce the
CC proliferation of neural cells and regeneration of nerve and brain tissue
CC and are useful for the treatment of central and peripheral nervous system
CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
CC Huntington's disease, amyotrophic lateral sclerosis (ALS). The
CC polypeptides are also involved in chemotactic or chemokinetic activity,
CC regulation of haematopoiesis and are useful for treating myeloid or
CC lymphoid cell disorders, platelet disorders such as thrombocytopaenia and
CC for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, in tissue repair, healing of burns, incisions, ulcers, for
CC treating osteoporosis, osteoarthritis, bone degenerative disorders, and
CC periodontal disease. The polypeptides are also useful for gut protection
CC or regeneration and treatment of lung or liver fibrosis, reperfusion
CC injury in various tissues, various immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid

CC arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and
 CC conditions, such as asthma or other respiratory problems. The
 CC polypeptides are involved in thrombolysis or thrombosis and are useful in
 CC treatment of various coagulation disorders (including hereditary
 CC disorders such as haemophilia) or to enhance coagulation and other
 CC haemostatic events in treating wounds resulting from trauma, surgery or
 CC other causes. The polypeptides exhibit immune stimulating or immune
 CC suppressing activity, and are useful for treating autoimmune diseases or
 CC cancer. They also inhibit the growth, infection or function of infectious
 CC agents such as bacteria, fungi, viruses, effect biophysics or circadian
 CC cycles of rhythms, fertility of male or female subjects, metabolism,
 CC cataplexy, and anabolism. ABO00414-ABO00749 represent the novel
 CC polypeptides of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC XX

SQ Sequence 167 AA;

Query Match

Best Local Similarity 56.5%; Score 52; DB 6; Length 167;
 Pred. No. 4.1;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WIMNQMHIDEKN 14
 | : | | | : | | |
 Db 45 WYMNQFVPEEN 57

Search completed: July 29, 2004, 11:34:54
 Job time : 48.6667 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:32:25 ; Search time 13 Seconds

(Without alignments)
59.568 Million cell updates/sec

Title: US-10-040-128-3

Sequence: 1 DWIMNQMHIIDEKNT 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCPUS COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	108	4	US-09-187-859-6
2	92	100.0	108	4	US-09-839-542B-6
3	92	100.0	108	4	US-09-535-852-6
4	92	100.0	780	1	US-08-188-228-50
5	92	100.0	780	1	US-08-332-643-44
6	92	100.0	780	1	US-08-332-638-50
7	92	100.0	780	1	US-09-187-859-13
8	49	53.3	110	4	US-09-839-542B-13
9	49	53.3	110	4	US-09-535-852-13
10	49	53.3	532	1	US-08-188-228-44
11	49	53.3	532	1	US-08-332-638-44
12	49	53.3	793	1	US-08-188-228-54
13	49	53.3	793	1	US-08-332-643-48
14	49	53.3	793	1	US-08-332-638-54
15	49	53.3	799	1	US-08-188-228-42
16	49	53.3	799	1	US-08-332-638-42
17	45	48.9	106	4	US-09-187-859-44
18	45	48.9	106	4	US-09-187-859-45
19	45	48.9	106	4	US-09-305-927-1
20	45	48.9	106	4	US-09-305-927-2
21	45	48.9	106	4	US-09-305-927-3
22	45	48.9	106	4	US-09-073-040-12
23	45	48.9	106	4	US-09-073-040-13
24	45	48.9	106	4	US-09-839-542B-44
25	45	48.9	106	4	US-09-839-542B-45
26	45	48.9	106	4	US-09-264-516A-1
27	45	48.9	106	4	US-09-264-516A-2

28	45	48.9	106	4	US-09-264-516A-3	Sequence 3, Appli
29	45	48.9	106	4	US-09-234-395-4	Sequence 4, Appli
30	45	48.9	106	4	US-09-234-395-5	Sequence 5, Appli
31	45	48.9	106	4	US-09-305-928-4	Sequence 4, Appli
32	45	48.9	106	4	US-09-305-928-5	Sequence 5, Appli
33	45	48.9	110	4	US-09-187-859-22	Sequence 4, Appli
34	45	48.9	110	4	US-09-187-859-22	Sequence 22, Appli
35	45	48.9	110	4	US-09-839-542B-4	Sequence 4, Appli
36	45	48.9	110	4	US-09-839-542B-22	Sequence 22, Appli
37	45	48.9	110	4	US-09-535-852-4	Sequence 4, Appli
38	45	48.9	110	4	US-09-535-852-22	Sequence 22, Appli
39	45	48.9	615	2	US-08-738-349-12	Sequence 12, Appli
40	45	48.9	615	2	US-08-738-349-6	Sequence 6, Appli
41	45	48.9	796	1	US-08-188-228-58	Sequence 58, Appli
42	45	48.9	796	1	US-08-332-643-52	Sequence 52, Appli
43	45	48.9	796	1	US-08-332-638-58	Sequence 58, Appli
44	45	48.9	796	2	US-08-738-349-2	Sequence 2, Appli
45	45	48.9	796	2	US-08-738-349-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-187-859-6
; Sequence 6, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-859-6

Query Match 100.0%; Score 92; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMNQMHIIDEKNT 15
DB 5 DWIMNQMHIIDEKNT 19

RESULT 2
US-09-839-542B-6
; Sequence 6, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-6

Query Match 100.0%; Score 92; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDEKNT 15
|||||
Db 5 DWIMQMHIDEKNT 19

RESULT 3
US-09-535-852-6

; Sequence 6, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-535-852-6

Query Match 100.0%; Score 92; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDEKNT 15
|||||
Db 5 DWIMQMHIDEKNT 19

RESULT 4
US-08-188-228-50

; Sequence 50, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-188-228-50

Query Match 100.0%; Score 92; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDEKNT 15
|||||
Db 44 DWIMQMHIDEKNT 58

RESULT 5
US-08-332-643-44

; Sequence 44, Application US/08332643
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-643-44

Query Match 100.0%; Score 92; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDEKNT 15
|||||

Db 44 DWIMNQHIDEKNT 58

```
RESULT 6
US-08-332-638-50
; Sequence 50, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borum
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TLEX: 25-3856
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-50
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```
Query Match 100.0%; Score 92; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DWIMNQHIDEKNT 15
Db 44 DWIMNQHIDEKNT 58
```

```
RESULT 7
US-09-187-859-13
; Sequence 13, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 13
```

```
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-859-13
```

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Query Match 53.3%; Score 49; DB 4; Length 110;
Best Local Similarity 63.6%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 WIMNQHIDE 12
Db 6 WIMNQHIDE 16
```

```
RESULT 8
US-09-839-542B-13
; Sequence 13, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-13
```

```
Query Match 53.3%; Score 49; DB 4; Length 110;
Best Local Similarity 63.6%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 WIMNQHIDE 12
Db 6 WIMNQHIDE 16
```

```
RESULT 9
US-09-535-852-13
; Sequence 13, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-852-13
```

```
Query Match 53.3%; Score 49; DB 4; Length 110;
Best Local Similarity 63.6%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 WIMNQHIDE 12
Db 6 WIMNQHIDE 16
```

RESULT 10
US-08-188-228-44
; Sequence 44, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-44

Query Match 53.3%; Score 49; DB 1; Length 532;
Best Local Similarity 63.6%; Pred. No. 8.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
DB 63 WYNNOMFVLEE 73

RESULT 11
US-08-332-638-44
; Sequence 44, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-44

Query Match 53.3%; Score 49; DB 1; Length 532;
Best Local Similarity 63.6%; Pred. No. 8.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
DB 63 WYNNOMFVLEE 73

RESULT 12
US-08-188-228-54
; Sequence 54, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 53.3%; Score 49; DB 1; Length 793;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
|:|||||: ||
56 WWINOMFVLEE 66

RESULT 13
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 53.3%; Score 49; DB 1; Length 793;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 WINNOMHIDE 12
|:|||||: ||

Db 56 WWINOMFVLEE 66

RESULT 14
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 53.3%; Score 49; DB 1; Length 793;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
|:|||||: ||
56 WWINOMFVLEE 66

RESULT 15
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 53.3%; Score 49; DB 1; Length 799;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 MINOMHIDE 12
|:|:|:|:|:|:|
Db 63 WWMNQMFVLEE 73

Search completed: July 29, 2004, 11:38:39
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:29:40 ; Search time 46.6667 Seconds

(without alignments)
90.819 Million cell updates/sec

Title: US-10-040-128-3

Sequence: 1 DWTNQMHIIDEKNT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	15	AAU08779	AAU08779 VE-cadher
2	92	100.0	4	AAU08785	AAU08785 Human VE-
3	92	100.0	108	AAV64578	AAV64578 Nonclassi
4	92	100.0	566	AAU11276	AAU11276 Human rec
5	92	100.0	594	AAU11279	AAU11279 Human rec
6	92	100.0	780	AAW25634	AAW25634 Human cad
7	92	100.0	780	AAW13130	AAW13130 Full leng
8	92	100.0	784	ABR81477	ABR81477 Human VE-
9	92	100.0	784	ABU03507	ABU03507 Angiogene
10	92	100.0	784	ABU03507	ABU03507 Angiogene
11	92	100.0	784	ADA03363	ADA03363 Human vas
12	87	94.6	15	AAU08778	AAU08778 VE-cadher
13	87	94.6	103	AAU08786	AAU08786 Murine VE
14	73	79.3	15	AAU08777	AAU08777 VE-cadher
15	57	62.0	167	ABO00590	ABO00590 Novel hum
16	57	62.0	772	AAV41725	AAV41725 Human PRO
17	57	62.0	772	AAV41725	AAV41725 Human PRO
18	57	62.0	772	AAV41725	AAV41725 Human PRO
19	57	62.0	772	AAV41725	AAV41725 Human PRO
20	57	62.0	772	AAV41725	AAV41725 Human PRO
21	57	62.0	772	AAV41725	AAV41725 Human PRO
22	57	62.0	772	AAV41725	AAV41725 Human PRO
23	57	62.0	772	AAV41725	AAV41725 Human PRO
24	57	62.0	772	AAV41725	AAV41725 Human PRO
25	57	62.0	772	AAV41725	AAV41725 Human PRO

26	57	62.0	772	6	ABU82758	ABU82758 Human PRO
27	57	62.0	772	6	ABU89879	ABU89879 Novel hum
28	57	62.0	772	6	ABR68128	ABR68128 Human sec
29	57	62.0	772	6	ABU96181	ABU96181 Novel hum
30	57	62.0	772	6	ABU92612	ABU92612 Human sec
31	57	62.0	772	6	ABO08689	ABO08689 Human sec
32	57	62.0	772	6	ABO02741	ABO02741 Human sec
33	57	62.0	772	6	ABR74895	ABR74895 Human sec
34	57	62.0	772	6	ABR94657	ABR94657 Human sec
35	57	62.0	772	6	ABO25180	ABO25180 Novel hum
36	57	62.0	772	6	ABO25227	ABO25227 Novel hum
37	57	62.0	772	6	ABU85630	ABU85630 Human PRO
38	57	62.0	772	6	ABU89790	ABU89790 Novel hum
39	57	62.0	772	6	ABU98005	ABU98005 Novel hum
40	57	62.0	772	6	ABU91711	ABU91711 Novel hum
41	57	62.0	772	6	ABU72233	ABU72233 Novel hum
42	57	62.0	772	6	ABU89404	ABU89404 Human PRO
43	57	62.0	772	6	ABU86245	ABU86245 Human sec
44	57	62.0	772	6	ABU67458	ABU67458 Human sec
45	57	62.0	772	6	ABU80486	ABU80486 Human PRO

ALIGNMENTS

RESULT 1
AAU08779
ID AAU08779 standard; peptide; 15 AA.
XX
AC AAU08779;
XX
DT 27-FEB-2002 (first entry)
XX
DE VE-cadherin N-terminal domain 1 antibody binding peptide #3.
XX
XX
XX VE-cadherin, antibody binding peptide; angiogenesis; neoplastic disease;
XX VE-cadherin mediated adherens junction formation; autoimmune disease;
XX paracrine permeability; solid tumour; collagenous vascular disease;
XX rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
XX retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
XX carcinoma; sarcoma; adenocarcinoma; adenoma; gene therapy;
XX leukaemic tumour; lymphoid tumours; cell proliferation disorder;
XX vascularisation; blood vessel proliferation disorder; fibrotic disorder;
XX age-related muscular degeneration; tumour neovascularisation;
XX VE-cadherin N-terminal domain 1.
XX
OS Mammalia.
XX
PN WO200175109-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US010505.
XX
PR 31-MAR-2000; 2000US-00540967.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Liao F, Hicklin DJ, Bohlen P;
XX WPI; 2001-656988/75.
XX
XX New antibody antagonists of VE-cadherin, which does not adversely affect
XX vascular permeability, useful for inhibiting angiogenesis or tumor
XX metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.
XX
PS Claim 1; Page 32; 44pp; English.
XX
XX The method relates to an antibody or an antibody fragment, capable of
XX specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
XX mediated adherens junction formation in vitro, but does not exert any
XX significant or substantial effect on paracrine permeability in vitro.
XX The antibody or antibody fragment is capable of specifically binding to a

CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
 CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
 CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
 CC disease, a solid tumour, an autoimmune disease, collagenous vascular
 CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
 CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
 CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas,
 CC adenocarcinomas, adenomas, leukaemic tumours or lymphoid tumours). The
 CC composition or antibody is also useful for treating a cell proliferation
 CC disorder associated with vascularisation (e.g. blood vessel proliferation
 CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
 CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
 CC These may also be used for reducing or inhibiting tumour vasculature in a
 CC mammal. The nucleic acid that encodes the antibody or is useful in gene
 CC therapy, particularly for inhibiting angiogenesis or tumour
 CC neovascularisation. This sequence represents a VE-cadherin N-terminal
 CC domain 1 antibody binding peptide

XX Sequence 15 AA;

SO Query Match 100.0%; Score 92; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.3e-07; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

OY 1 DWIMNQHIDEKNT 15
 DB 1 DWIMNQHIDEKNT 15

RESULT 2

AA08785 standard; protein; 104 AA.

XX AA08785;

DT 27-FEB-2002 (first entry)

XX Human VE-cadherin N-terminal domain 1 polypeptide.

XX VE-cadherin; angiogenesis; neoplastic disease;
 XX VE-cadherin mediated adherens junction formation; autoimmune disease;
 XX paracellular permeability; solid tumour; collagenous vascular disease;
 XX rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
 XX retrolental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
 XX carcinoma; sarcoma; adenocarcinoma; adenoma; gene therapy;
 XX leukaemic tumour; lymphoid tumours; cell proliferation disorder;
 XX leukaemia; blood vessel proliferation disorder; fibrotic disorder;
 XX age-related muscular degeneration; tumour neovascularisation; human;
 XX VE-cadherin N-terminal domain 1.

XX Homo sapiens.

XX WO200175109-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US010505.

PR 31-MAR-2000; 2000US-00540967.

XX (IMCL-) IMCLONE SYSTEMS INC.

PI Liao F, Hicklin DJ, Bohlen P;

XX WPI; 2001-656988/75.

XX New antibody antagonists of VE-cadherin, which does not adversely affect
 XX vascular permeability, useful for inhibiting angiogenesis or tumour
 XX metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.

XX Example 2; Fig 2; 4pp; English.

XX The method relates to an antibody or an antibody fragment, capable of

CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
 CC mediated adherens junction formation in vitro, but does not exert any
 CC significant or substantial effect on paracellular permeability in vitro.
 CC The antibody or antibody fragment is capable of specifically binding to a
 CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
 CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
 CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
 CC disease, a solid tumour, an autoimmune disease, collagenous vascular
 CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
 CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
 CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas,
 CC adenocarcinomas, adenomas, leukaemic tumours or lymphoid tumours). The
 CC composition or antibody is also useful for treating a cell proliferation
 CC disorder associated with vascularisation (e.g. blood vessel proliferation
 CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
 CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
 CC These may also be used for reducing or inhibiting tumour vasculature in a
 CC mammal. The nucleic acid that encodes the antibody or is useful in gene
 CC therapy, particularly for inhibiting angiogenesis or tumour
 CC neovascularisation. This sequence represents a human VE-cadherin N-
 CC terminal domain 1 polypeptide

XX Sequence 104 AA;

SO Query Match 100.0%; Score 92; DB 4; Length 104;

Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

OY 1 DWIMNQHIDEKNT 15
 DB 1 DWIMNQHIDEKNT 15

RESULT 3

AA64578 standard; peptide; 108 AA.

XX AA64578;

DT 02-MAR-2000 (first entry)

XX Nonclassical cadherin extracellular domain SEQ ID NO:6.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 XX inhibition; cadherin extracellular domain; cell adhesion recognition;
 XX OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 XX cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 XX cadherin related neuronal receptor; LI-cadherin; protocadherin;
 XX desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 XX rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 XX neurological disease.

XX Mammalia.

XX WO9957149-A2.

PD 11-NOV-1999.

PF 05-MAY-1999; 99WO-CA000363.

PR 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin

XX mediated functions for treating e.g. cancers, obesity, rheumatoid

PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Disclosure; Fig 2; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY64572 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
SQ
Sequence 108 AA;
Query Match 100.0%; Score 92; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DWIMQMHIDEKNT 15
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
DB 5 DWIMQMHIDEKNT 19
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
RESULT 4
AAU11276
ID AAU11276 standard; protein; 566 AA.
XX
AC AAU11276;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human recombinant KVE702 polypeptide.
XX
KW Human; KV protein; KVE702; angiogenic factor antagonist; angiogenesis;
KW vascular endothelial structure regulator; cancer; vascular endothelium;
KW tumour; blood vessel; epithelial cell; cytosstatic; gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
WO200183562-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-GB001956.
XX
PR 04-MAY-2000; 2000GB-00010630.
XX
PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
PI Jiang WG;
XX
PI
XX
DR MPI; 2002-066521/09.
DR N-PSDB; AAS16965.
XX
PT Novel nucleic acid for inhibition of angiogenesis and prophylaxis or
PT treatment of cancer, comprises both an angiogenic factor antagonist and a

PT vascular endothelial structure regulator.
XX
PS Disclosure; Fig 2; 66pp; English.
XX
CC The invention relates to recombinant nucleic acid sequences that encode
CC both an angiogenic factor antagonist and a vascular endothelial structure
CC regulator, collectively referred to as a KV protein. KV DNA and proteins,
CC and also cells and compositions containing the sequences, are useful in
CC treating or preventing cancer or angiogenesis in mammals, in particular
CC humans. KV proteins are also useful for regulation of the development of
CC blood vessels and their formation, in the vascular endothelium and/or
CC tumour. The KVE702 gene and its fragments are useful in transfection of
CC human epithelial cells and to generate products suitable for angiogenesis
CC intervention. This sequence represents the human KVE702 protein
SQ
Sequence 566 AA;
Query Match 100.0%; Score 92; DB 5; Length 566;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DWIMQMHIDEKNT 15
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
DB 474 DWIMQMHIDEKNT 488
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
RESULT 5
AAU11279
ID AAU11279 standard; protein; 594 AA.
XX
AC AAU11279;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human recombinant J37 polypeptide.
XX
KW Human; KV protein; KVE702; angiogenic factor antagonist; angiogenesis;
KW vascular endothelial structure regulator; cancer; vascular endothelium;
KW tumour; blood vessel; epithelial cell; cytosstatic; gene therapy; J37.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Misc-difference 518
FT FT /note= "Encoded by ATC"
XX
PN WO200183562-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-GB001956.
XX
PR 04-MAY-2000; 2000GB-00010630.
XX
PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
PI Jiang WG;
XX
PI
XX
DR MPI; 2002-066521/09.
DR N-PSDB; AAS16975.
XX
PT Novel nucleic acid for inhibition of angiogenesis and prophylaxis or
PT treatment of cancer, comprises both an angiogenic factor antagonist and a
PT vascular endothelial structure regulator.
XX
PS Disclosure; Fig 15; 66pp; English.
XX
CC The invention relates to recombinant nucleic acid sequences that encode
CC both an angiogenic factor antagonist and a vascular endothelial structure
CC regulator, collectively referred to as a KV protein. KV DNA and proteins,
CC and also cells and compositions containing the sequences, are useful in
CC treating or preventing cancer or angiogenesis in mammals, in particular

CC humans. KV proteins are also useful for regulation of the development of
 CC blood vessels and their formation, in the vascular endothelium and/or
 CC tumour. The KVE702 gene and its fragments are useful in transfection of
 CC human epithelial cells and to generate products suitable for angiogenesis
 CC intervention. This sequence represents the human J37 protein used in
 CC methods of the invention

XX Sequence 594 AA;

Query Match 100.0%; Score 92; DB 5; Length 594;

Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWTWQMHIDEKNT 15
 |||||
 DB 49 DWTWQMHIDEKNT 63

RESULT 6

AAW25634
 ID AAW25634 standard; protein; 780 AA.

XX AAW25634;

DT 25-MAR-2003 (revised)
 DT 03-NOV-1997 (first entry)

XX Human cadherin-5.

XX Human; cadherin; rat; calcium-dependent cell adhesion protein;
 KW superfamily; cytoskeleton; eatenin; cancer.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 622

FT /note= "encoded by AAG"

XX US5646250-A.

XX 08-JUL-1997.

PF 01-NOV-1994; 94US-00332638.

PR 17-APR-1992; 92US-00872643.

PR 19-APR-1993; 93US-00049460.

XX (DOHE-) DOHENY EYE INST.

XX Suzuki S;

XX WPI; 1997-362997/33.

XX N-PSDB; AAT85401.

XX Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion.

XX Claim 1; Col 69-72; 56pp; English.

XX This sequence represents human cadherin-5. The invention specifically
 CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat
 CC cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell
 CC adhesion proteins. They are glycosylated integral membrane proteins that
 CC have an N-terminal extracellular domain that determines binding
 CC specificity, a hydrophobic membrane spanning region and a C-terminal
 CC cytoplasmic domain, which is highly conserved among members of the
 CC superfamily. The C-terminal domain interacts with the cytoskeleton
 CC through eatenins and other cytoskeleton-associated proteins. The novel
 CC cadherin proteins may be used in the analysis of the role of cadherins in
 CC various cancers. Sequence analysis of the cadherin proteins also allows
 CC investigation of the structure and function of cadherin. The cadherin
 CC proteins may be isolated by using anti-cadherin antibodies. These
 CC antibodies may also be used to modulate the activity of cadherin and to
 CC determine the tissue specific distribution of cadherin proteins. Each

CC subclass of cadherins has a unique tissue distribution pattern. (Updated
 CC on 25-MAR-2003 to correct PF field.)

XX Sequence 780 AA;

QY Query Match 100.0%; Score 92; DB 2; Length 780;

Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWTWQMHIDEKNT 15
 |||||
 DB 44 DWTWQMHIDEKNT 58

RESULT 7

AAW13130
 ID AAW13130 standard; protein; 780 AA.

XX AAW13130;

DT 25-MAR-2003 (revised)
 DT 13-MAY-1997 (first entry)

XX Full length human cadherin-5.

XX Ca2+ dependent; cell adhesion protein; placental; cadherin; rat; brain;
 KW human; antibody; purification; determination; tissue expression;
 KW binding antagonist; calcium ion.

XX Homo sapiens.

XX US5597725-A.

XX 28-JAN-1997.

PF 26-JAN-1994; 94US-00188228.

PR 17-APR-1992; 92US-00872643.

PR 19-APR-1993; 93US-00049460.

XX (DOHE-) DOHENY EYE INST.

XX Suzuki S;

XX WPI; 1997-108328/10.

XX N-PSDB; AAT61921.

XX Antibodies to cadherin proteins - useful as cadherin antagonists, etc.

XX Claim 5; Col 75-78; 59pp; English.

XX The present sequence is full length human cadherin-5, which is a Ca2+
 CC dependent cell adhesion protein. The human cadherin cDNA was isolated
 CC from a placental cDNA library, using probes based on homologous rat
 CC cadherin cDNA. Antibodies or fragments that specifically bind the human
 CC cadherin can be used to purify the cadherin, determine its tissue
 CC expression and antagonise its ligand/antiligand binding activities.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 780 AA;

Query Match 100.0%; Score 92; DB 2; Length 780;

Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWTWQMHIDEKNT 15
 |||||
 DB 44 DWTWQMHIDEKNT 58

RESULT 8

ABB81477
 ID ABB81477 standard; protein; 784 AA.

[illegible]

```

XX 21-JUN-2003 (first entry)
XX
XX Angiogenesis-associated human protein sequence #52.
DE
XX Human, angiogenesis-associated transcript; angiogenesis;
KM angiogenesis-associated disease; cancer; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200279492-A2.
PN
PD 10-OCT-2002.
PF
XX 14-FEB-2002; 2002WO-US004915.
XX
XX 14-FEB-2001; 2001US-00784356.
PR 22-FEB-2001; 2001US-00791390.
PR 19-APR-2001; 2001US-0285475P.
PR 03-AUG-2001; 2001US-0310025P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334244P.
PA
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PI
XX Murray R, Glynn R, Watson SR, Aziz N;
XX
XX MPI; 2003-040681/03.
DR N-PDSB; ABX08791.
XX
XX Detecting angiogenesis-associated transcript in a cell for diagnosing and
PT treating cancer by contacting a sample with a polynucleotide that
PT exhibits changes in expression level as a function of time in tissue
PT undergoing angiogenesis.
XX
XX Example 2; Page 230; 291pp; English.
XX
XX The present invention relates to methods and compositions for detecting
CC an angiogenesis-associated transcript in a cell in a patient. The method
CC involves contacting a biological sample from the patient with a
CC polynucleotide that selectively hybridises to a sequence at least 80%
CC identical to any of the angiogenesis-associated human polynucleotide
CC sequences given in the specification. These angiogenesis-associated
CC polynucleotide sequences comprise genes that exhibit changes in
CC expression levels as a function of time in tissue undergoing
CC angiogenesis. The method and the polynucleotide sequences of the
CC invention are useful for diagnosing and treating angiogenesis and
CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
CC sequences are also useful in the gene therapy of such disorders. The
CC angiogenesis-associated proteins encoded by the polynucleotide sequences
CC are useful as a vaccine for therapeutic and prophylactic immunisation.
CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences
XX
XX
SQ Sequence 784 AA;

```

XX lung cancer-associated polypeptide; cytosolic; emphysema;
XX anti-inflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
PI Aziz N, Murray R;
DR WPI; 2003-093161/08.
DR N-PDDB; ABX76299.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 314; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, and
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX

SQ Sequence 784 AA;

QY Query Match 100.0%; Score 92; DB 6; Length 784;
Best Local Similarity 100.0%; Pred No. le-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Db 1 DWTWQMHIIDEKNT 15
|||||
48 DWIMQMHIIDEKNT 62

RESULT 11
ADA03363
ID ADA03363 standard; protein; 784 AA.
AC ADA03363;
XX

06-NOV-2003 (first entry)
 Human vascular endothelial cadherin protein.
 cyostatic; antidiabetic; ophthalmological; antiarthritic;
 endostatin receptor; angiogenesis inhibitor; human;
 vascular endothelial cadherin; angiogenesis; blood vessel; cancer;
 diabetic retinopathy; rheumatoid arthritis; receptor.
 Homo sapiens.
 WC2003038096-A1.
 08-MAY-2003.
 28-OCT-2002; 2002W0-JP011143.
 30-OCT-2001; 2001JP-00333295.
 (KUBO/) KUBOTA S.
 (MEMO/) MEMOTO T.
 Kubota S, Nemoto T;
 WPI, 2003-430528/40.
 N-PSDB; ADA03362.
 Vascular endothelial cadherin is a receptor to endostatin for screening
 endostatin agonists and antagonists as angiogenesis inhibitors and
 remedies for cancer development and proliferation.
 Claim 2; Page 44-47; 56pp; Japanese.
 The invention relates to a DNA encoding an endostatin receptor protein
 (human vascular endothelial (VE) cadherin (IT)) or its partial peptides or
 encoding a protein derived from (I) by addition, deletion or substitution
 of one or more amino acid residues and having similar binding activity to
 endostatin. The sequence can be used in the regulation of angiogenesis in
 the treatment and prevention of diseases associated with the formation of
 new blood vessels, including cancer, cancer proliferation, diabetic
 retinopathy and rheumatoid arthritis. This sequence corresponds to the VE
 cadherin protein which serves as an endostatin receptor protein.
 Sequence 784 AA;
 Query Match 100.0%; Score 92; DB 6; Length 784;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 1 DWIWMQHIDEKNT 15
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 48 DWIWMQHIDEKNT 62
 RESULT 12
 AAU08778
 AAU08778 standard; peptide; 15 AA.
 AAU08778;
 27-FEB-2002 (first entry)
 VE-cadherin N-terminal domain 1 antibody binding peptide #2.
 VE-cadherin; antibody binding peptide; angiogenesis; neoplastic disease;
 VE-cadherin mediated adherens junction formation; autoimmune disease;
 paracellular permeability; solid tumour; collagenous vascular disease;
 rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
 retinental fibroplasia; neovascular glaucoma; tumour metastasis; glioma;
 carcinoma; sarcoma; adenocarcinoma; adenocarcinoma; adenoma; gene therapy;
 leukemic tumour; lymphoid tumours; cell proliferation disorder;
 vascularisation; blood vessel proliferation disorder; fibrotic disorder;
 age-related muscular degeneration; tumour neovascularisation;

XX VE-cadherin mediated adherens junction formation; autoimmune disease;
 KW paracellulular permeability; solid tumor; collagenous vascular disease;
 KW rheumatoid arthritis; ophthalmological condition; diabetic retinopathy;
 KW retrolental fibroplasia; neovascular glaucoma; tumor metastasis; glioma;
 KW carcinoma; sarcoma; adenocarcinoma; adenocarcinoma; adenoma; gene therapy;
 KW leukemic tumor; lymphoid tumors; cell proliferation disorder;
 KW vasculatization; blood vessel proliferation disorder; fibrotic disorder;
 KW age-related muscular degeneration; tumor neovascularization;
 KW VE-cadherin N-terminal domain 1.
 XX
 OS Mammalia.
 XX
 PN WO200175109-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US010505.
 XX
 PR 31-MAR-2000; 2000US-00540967.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Liao F, Hicklin DJ, Bohlen P;
 XX
 DR WPI; 2001-656988/75.
 XX
 PT New antibody antagonists of VE-cadherin, which does not adversely affect
 PT vascular permeability, useful for inhibiting angiogenesis or tumor
 PT metastasis, e.g. autoimmune disease, carcinomas or leukemic tumors.
 XX
 PS Claim 1; Page 32; 4app; English.
 XX
 CC The method relates to an antibody or an antibody fragment, capable of
 CC specifically binding to a VE-cadherin, and of inhibiting VE-cadherin
 CC mediated adherens junction formation in vitro, but does not exert any
 CC significant or substantial effect on paracellulular permeability in vitro.
 CC The antibody or antibody fragment is capable of specifically binding to a
 CC site on a VE-cadherin within the 15 N-terminal amino acids of domain 1 of
 CC a VE-cadherin. The antibody or antibody fragment is useful for inhibiting
 CC angiogenesis (e.g. angiogenesis that is associated with a neoplastic
 CC disease, a solid tumour, an autoimmune disease, collagenous vascular
 CC disease, rheumatoid arthritis, an ophthalmological condition, diabetic
 CC retinopathy, retrolental fibroplasia or neovascular glaucoma) or tumour
 CC metastasis (e.g. carcinomas, gliomas, sarcomas, adenocarcinomas, The
 CC adenocarcinomas, adenomas, leukemic tumours or lymphoid tumours). The
 CC composition or antibody is also useful for treating a cell proliferation
 CC disorder associated with vascularisation (e.g. blood vessel proliferation
 CC disorders, fibrotic disorders, angiogenesis, tumour growth, tumour
 CC metastasis, rheumatoid arthritis or age-related muscular degeneration).
 CC These may also be used for reducing or inhibiting tumour vasculature in a
 CC mammal. The nucleic acid that encodes the antibody or is useful in gene
 CC therapy, particularly for inhibiting angiogenesis or tumour
 CC neovascularisation. This sequence represents a VE-cadherin N-terminal
 CC domain 1 antibody binding peptide
 XX
 XX Sequence 15 AA:
 XX
 SQ
 Query Match 79.3%; Score 73; DB 4; Length 15;
 Best Local Similarity 92.9%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DWTINQMHIIDEKN 14
 DB 1 DEIMNQMHIDEKN 14
 RESULT 15
 ABO000590 standard; protein; 167 AA.
 ID ABO000590
 AC ABO000590;
 XX
 DT 06-AUG-2003 (first entry)

XX
 DE Novel human polypeptide #177.
 XX
 KW Human; angiogenesis; cytokine; cell proliferation; pluripotent;
 KW cell differentiation; totipotent; stem cell; transplantation; bio-sensor;
 KW neuroepithelial cell; autoimmune disease; neural cell; genetic disorder;
 KW nerve; brain tissue; central nervous system disease;
 KW peripheral nervous system disease; neuropathy; haematopoiesis; bone;
 KW myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;
 KW regeneration; cartilage; tendon; ligament; nerve tissue growth;
 KW tissue repair; wound healing; burn ulcer; osteoporosis; cancer;
 KW osteoarthritis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung fibrosis; liver fibrosis; reperfusion injury;
 KW immune deficiency; infection; autoimmune disorder; allergic reaction;
 KW thrombolytic; thrombosis; coagulation disorder; hereditary disorder;
 KW biortym; circadian cycle; fertility; metabolism; catabolism; anabolism;
 KW neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
 KW haemostatic; vulnerrary; antilucer; osteopathic; antiarthritic;
 KW vasotrophic; immunostimulant; antibacterial; fungicide; immunosuppressive;
 KW antirheumatic; antidiabetic; antisthmatic; cytostatic; virucide.
 XX
 OS Homo sapiens.
 XX
 PN WO2003023013-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 13-SEP-2002; 2002WO-US029001.
 XX
 PR 13-SEP-2001; 2001US-0322511P.
 XX
 PR 12-SEP-2002; 2002US-00243552.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;
 XX
 DR WPI; 2003-312249/30.
 DR N-PSDB; ACD05667.
 XX
 PT Novel nucleic acids and polypeptides for diagnosis, treatment of central
 PT and peripheral nervous system diseases and neuropathies, such as
 PT Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 PT lateral sclerosis.
 XX
 PS Claim 20; SEQ ID NO 513; 300pp; English.
 XX
 CC The present invention relates to the isolation of novel human
 CC polynucleotide sequences and their encoding polypeptides. The novel
 CC polypeptides exhibit activities relating to angiogenesis, cytokine, cell
 CC proliferation, cell differentiation, antiinflammatory, and stem cell
 CC growth factor activities. The polypeptides are involved in the
 CC proliferation, differentiation and survival of pluripotent and totipotent
 CC stem cells, and are useful for re-engineering damaged or diseased
 CC tissues, transplantation, manufacture of bio-pharmaceuticals and
 CC development of bio-sensors. The polypeptides can be used to manipulate
 CC stem cells in culture to give rise to neuroepithelial cells that can be
 CC used to augment or replace cells damaged by illness, autoimmune disease,
 CC accidental damage or genetic disorders. The polypeptides induce the
 CC proliferation of neural cells and regeneration of nerve and brain tissue
 CC and are useful for the treatment of central and peripheral nervous system
 CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
 CC Huntington's disease, amyotrophic lateral sclerosis (ALS). The
 CC polypeptides are also involved in chemotactic or chemokinetic activity,
 CC regulation of haematopoiesis and are useful for treating myeloid and
 CC lymphoid cell disorders, platelet disorders such as thrombocytopenia and
 CC for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, in tissue repair, healing of burns, incisions, ulcers, for
 CC treating osteoporosis, osteoarthritis, bone degenerative disorders, and
 CC periodontal disease. The polypeptides are also useful for gut protection
 CC or regeneration and treatment of lung or liver fibrosis, reperfusion
 CC injury in various tissues, various immune deficiencies and disorders
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid

CC arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and
 CC conditions, such as asthma or other respiratory problems. The
 CC polypeptides are involved in thrombolysis or thrombosis and are useful in
 CC treatment of various coagulation disorders (including hereditary
 CC disorders such as haemophilia) or to enhance coagulation and other
 CC haemostatic events in treating wounds resulting from trauma, surgery or
 CC other causes. The polypeptides exhibit immune stimulating or immune
 CC suppressing activity, and are useful for treating autoimmune diseases or
 CC cancer. They also inhibit the growth, infection or function of infectious
 CC agents such as bacteria, fungi, viruses, effect biorythms or circadian
 CC cycles of rhythms, fertility of male or female subjects, metabolism,
 CC catabolism, and anabolism. AB000414-AB000749 represent the novel
 CC polypeptides of the invention. Note: The sequence data for this patent
 CC did not form part of the invention. Note: The sequence data for this patent
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 167 AA;

Query Match 62.0%; Score 57; DB 6; Length 167;

Best Local Similarity 57.1%; Pred. No. 0.54;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 MWNQMHIDEKNT 15
 Db 45 MWNQPFVPEEMNT 58

Search completed: July 29, 2004, 11:34:54
 Job time : 46.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:37:16 ; Search time 38.333 Seconds

(without alignments)
122.745 Million cell updates/sec

Title: US-10-040-128-3

Perfect score: 92

Sequence: 1 DWIMNQHIDEKNT 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues
Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	15	US-10-040-128-3	Sequence 3, Appli
2	92	100.0	108	US-10-006-869-6	Sequence 6, Appli
3	92	100.0	108	US-10-395-032-6	Sequence 6, Appli
4	92	100.0	784	US-09-905-983-52	Sequence 52, Appli
5	92	100.0	784	US-10-211-462-105	Sequence 105, Appli
6	92	100.0	784	US-10-021-660-99	Sequence 99, Appli
7	92	100.0	784	US-10-174-677-23	Sequence 23, Appli
8	87	94.6	15	US-10-040-128-1	Sequence 1, Appli
9	73	79.3	15	US-10-040-128-1	Sequence 1, Appli
10	57	62.0	167	US-10-243-552-596	Sequence 596, Appli
11	57	62.0	772	US-09-978-295A-264	Sequence 264, App
12	57	62.0	772	US-09-978-687-264	Sequence 264, App
13	57	62.0	772	US-09-978-193A-264	Sequence 264, App
14	57	62.0	772	US-09-978-188A-264	Sequence 264, App
15	57	62.0	772	US-09-999-832A-264	Sequence 264, App

16	57	62.0	772	10	US-09-978-608A-264	Sequence 264, App
17	57	62.0	772	10	US-09-978-585A-264	Sequence 264, App
18	57	62.0	772	10	US-09-978-191A-264	Sequence 264, App
19	57	62.0	772	10	US-09-978-103A-264	Sequence 264, App
20	57	62.0	772	10	US-09-978-564A-264	Sequence 264, App
21	57	62.0	772	10	US-09-999-833A-264	Sequence 264, App
22	57	62.0	772	10	US-09-981-915A-264	Sequence 264, App
23	57	62.0	772	10	US-09-978-824A-264	Sequence 264, App
24	57	62.0	772	10	US-09-918-585A-264	Sequence 264, App
25	57	62.0	772	10	US-09-978-423A-264	Sequence 264, App
26	57	62.0	772	10	US-09-978-187A-264	Sequence 264, App
27	57	62.0	772	10	US-09-978-757A-264	Sequence 264, App
28	57	62.0	772	10	US-09-999-830A-264	Sequence 264, App
29	57	62.0	772	10	US-09-978-187A-264	Sequence 264, App
30	57	62.0	772	10	US-09-978-643A-264	Sequence 264, App
31	57	62.0	772	10	US-09-978-375A-264	Sequence 264, App
32	57	62.0	772	10	US-09-978-299A-264	Sequence 264, App
33	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
34	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
35	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
36	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
37	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
38	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
39	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
40	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
41	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
42	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
43	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
44	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App
45	57	62.0	772	10	US-09-978-188A-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-10-040-128-3
; Sequence 3, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Iao, Fang
; APPLICANT: Hicklin, Daniel J.
; APPLICANT: Bohlen, Peter
; TITLE OF INVENTION: Antibody Antagonists of VE-Cadherin Without Adverse Effects on
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-3

Query Match 100.0%; Score 92; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMNQHIDEKNT 15
|||
DB 1 DWIMNQHIDEKNT 15
|||

RESULT 2
US-10-006-869-6
; Sequence 6, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

```

; APPLICANT: Symonds, James Matthew
; APPLICANT: Gout, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-869-6

Query Match          100.0%; Score 92; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DWIMNQHIDEKNT 15
Db      5 DWIMNQHIDEKNT 19

RESULT 3
US-10-395-032-6
; Sequence 6, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gout, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-395-032-6

Query Match          100.0%; Score 92; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DWIMNQHIDEKNT 15
Db      5 DWIMNQHIDEKNT 19

RESULT 4
US-09-905-983-52
; Sequence 52, Application US/09905983
; Patent No. US20020045591A1
; GENERAL INFORMATION:
; APPLICANT: Geiger, Benjamin
; APPLICANT: Ben-Ze'ev, Avri
; APPLICANT: Sadot, Einar
; TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
; FILE REFERENCE: 01/22326
; CURRENT APPLICATION NUMBER: US/09/905,983
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 52
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-983-52

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Query Match          100.0%; Score 92; DB 9; Length 784;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DWIMNQHIDEKNT 15
Db      48 DWIMNQHIDEKNT 62

RESULT 5
US-10-211-462-105
; Sequence 105, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natsana
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-105

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Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DWIMNQHIDEKNT 15
Db      48 DWIMNQHIDEKNT 62

RESULT 6
US-10-021-660-99
; Sequence 99, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 784

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;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-021-660-99

Query Match

Best Local Similarity 100.0%; Score 92; DB 14; Length 784;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWINOMHIDEKNT 15
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Db 48 DWINOMHIDEKNT 62

RESULT 7

US-10-174-677-23
; Sequence 23, Application US/10174677
; Publication No. US20030190704A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Ting
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANCHORING STEM CELLS IN A MICROENVIR
; FILE REFERENCE: 40716 (IP-012)
; CURRENT APPLICATION NUMBER: US/10/174,677
; CURRENT FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-677-23

Query Match

Best Local Similarity 100.0%; Score 92; DB 14; Length 784;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWINOMHIDEKNT 15
|||
Db 48 DWINOMHIDEKNT 62

RESULT 8

US-10-040-128-2
; Sequence 2, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang
; APPLICANT: Hicklin, Daniel J.
; APPLICANT: Bohlen, Peter
; TITLE OF INVENTION: Antibody Antagonists of VE-Cadherin Without Adverse Effects on
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-2

Query Match 94.6%; Score 87; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWINOMHIDEKNT 14
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Db 1 DWINOMHIDEKNT 14

RESULT 9

US-10-040-128-1
; Sequence 1, Application US/10040128
; Publication No. US20020160003A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Fang
; APPLICANT: Hicklin, Daniel J.
; APPLICANT: Bohlen, Peter
; TITLE OF INVENTION: Antibody Antagonists of VE-Cadherin Without Adverse Effects on
; FILE REFERENCE: 11245/46976
; CURRENT APPLICATION NUMBER: US/10/040,128
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-040-128-1

Query Match 79.3%; Score 73; DB 13; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.00049;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DWINOMHIDEKNT 14
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Db 1 DWINOMHIDEKNT 14

RESULT 10

US-10-243-552-596
; Sequence 596, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Ma, Yunding
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pt_Fl_genes Version 5.0
; SEQ ID NO 596
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-243-552-596

Query Match	62.0%;	Score 57;	DB 12;	Length 167;
Best Local Similarity	57.1%;	Pred. No. 1.1;		
Matches	8;	Conservative	2;	Mismatches 4;
				Indels 0;
				Gaps 0.

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QY      2 W I W N Q M H I D E E K N T 15
         | : | | | : | | | |
Db      45 W W W N Q F F V P E E M N T 58
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RESULT 11
MS-09-978

US03-978,295A 28-
Sequence 264, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Prior Filing Date:	1998-04-22

PRIOR APPLICATION NUMBER: 60/082796
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.0%; Score 57; DB 9; Length 772;
Best Local Similarity 57.1%; Pred. No. 4.6;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
2 WNMWMIIDEKNT 15

Db 45 WNMWQFVPEEMNT 58
RESULT 12
US-09-978-697-264
Sequence 264, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.0%; Score 57; DB 9; Length 772;
 Best Local Similarity 57.1%; Pred. No. 4.6;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WIMNWHIDEKNT 15
 Db 45 WWMNDFVDEKNT 58

RESULT 13
 US-09-978-192A-264
 ; Sequence 264, Application US/09978192A

Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083545
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.0%; Score 57; DB 9; Length 772;
 Best Local Similarity 57.1%; Pred. No. 4.6; 4; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 0;

QY 2 WTWNCMHIDEKNT 15
 DB 45 WYWNOPFVEPENT 58

RESULT 14
 US-09-999-832A-264
 Sequence 264, Application US/09999832A
 Publication No. US20020192706A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan

APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Rong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C63
 CURRENT APPLICATION NUMBER: US/09/999,832A
 CURRENT FILING DATE: 2001-10-24
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 PRIOR FILING DATE: 2001-07-30
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Query Match      62.0%; Score 57; DB 9; Length 772;
Best Local Similarity 57.1%; Pred. No. 4.6;
Matches      8; Conservative      2; Mismatches      4; Indels      0; Gaps      0;

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Db      45 WWMQFVPEEMNT 58

RESULT 15
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; GENERAL INFORMATION:
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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, Audrey

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, V. Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
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; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/085697

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Query Match      62.0%; Score 57; DB 10; Length 772;
Best Local Similarity 57.1%; Pred. No. 4.6;
Matches      8; Conservative      2; Mismatches      4; Indels      0; Gaps      0;
QY      2 WTMNQMHIDEKNT 15
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Db      45 WTMNQFVPEKNT 58

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Search completed: July 29, 2004, 11:50:33
 Job time : 39.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 11:30:30 ; Search time 6.66667 Seconds

(without alignments)
117.158 Million cell updates/sec

Title: US-10-040-128-2

Sequence: 92
1 DWIMQMHIDEKNE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	784	1	CAD5_MOUSE
2	87	94.6	782	1	CAD5_PIG
3	87	94.6	784	1	CAD5_HUMAN
4	52	56.5	772	1	CAD7_HUMAN
5	49	53.3	799	1	CAD8_HUMAN
6	49	53.3	799	1	CAD8_MOUSE
7	49	53.3	799	1	CAD8_RAT
8	47.5	51.6	388	1	YD8A_BACSU
9	45	48.9	792	1	CAD8_CHICK
10	45	48.9	796	1	CAD8_MOUSE
11	45	48.9	796	1	CAD8_MOUSE
12	45	48.9	813	1	CAD8_MOUSE
13	45	48.9	813	1	CAD8_MOUSE
14	45	48.9	813	1	CAD8_MOUSE
15	45	48.9	813	1	CAD8_MOUSE
16	44	47.8	785	1	CAD7_CHICK
17	44	47.8	785	1	CAD7_CHICK
18	44	47.8	790	1	CAD7_HUMAN
19	44	47.8	794	1	CAD7_HUMAN
20	44	47.8	801	1	CAD7_HUMAN
21	43	46.7	435	1	HISX_BUCAL
22	42	45.7	427	1	CRISY_SALTY
23	41.5	45.1	789	1	NIRKX_ECOLI
24	41	44.6	314	1	NIRKX_ECOLI
25	41	44.6	363	1	DR3X_BUCAL
26	41	44.6	547	1	SPAK_HUMAN
27	41	44.6	553	1	SPAK_HUMAN
28	41	44.6	556	1	SPAK_HUMAN
29	41	44.6	788	1	CADA_MOUSE
30	41	44.6	789	1	CAD6_RAT
31	41	44.6	789	1	CAD6_RAT
32	41	44.6	790	1	CAD6_CHICK
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34	40.5	44.0	230	1	T2E7_ECOLI	P50194 escherichia
35	40.5	44.0	757	1	IKKB_MOUSE	O98351 mus musculus
36	40.5	44.0	757	1	IKKB_RAT	Q9978 ratius norv
37	40	43.5	146	1	HBBC_HOPI	P82316 hoplosternu
38	40	43.5	373	1	LYSI_YEAST	P38998 saccharomyc
39	40	43.5	418	1	GLYA_STRP3	O8K798 streptococc
40	40	43.5	418	1	GLYA_STRP8	O8P122 streptococc
41	40	43.5	418	1	GLYA_STRP5	O99221 streptococc
42	40	43.5	423	1	UROC_MOUSE	P06869 mus musculus
43	40	43.5	475	1	PRM2_ARATH	Q94410 arabidopsi
44	40	43.5	508	1	TNSD_ECOLI	P13991 escherichia
45	40	43.5	560	1	CALX_SCHPO	P35681 schistosach

ALIGNMENTS

RESULT 1
ID CAD5_MOUSE STANDARD; PRT; 784 AA.
AC P55284; O35542;
DT 01-OCT-1996 (Rel. 34, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain capillary;
RX MEDLINE=96141083; PubMed=8555485;
RA Breier G., Breviario F., Cavada L., Berthier R., Schnerch H.,
RT Gotsch U., Westweber D., Risau W., Dejana E.;
RT "Molecular cloning and expression of murine vascular endothelial-
RT cadherin in early stage development of cardiovascular system.";
RT Blood 87:630-641(1996).
RN (2)
RP REVISIONS TO 67-70.
RA Breviario F.;
RN Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=BALB/c; TISSUE=Breast carcinoma;
RX MEDLINE=97364256; PubMed=9220534;
RA Matsuyoshi N., Toda K.-I., Horiguchi Y., Tanaka T., Nakagawa S.,
RT Takeuchi M., Imanura S.;
RT "In vivo evidence of the critical role of cadherin-5 in murine
RT vascular integrity.";
RT Proc. Assoc. Am. Physicians 109:362-371(1997).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano L.N., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Garcia A.M., Gay L.J., Huliy S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X83930; CAA58782.2; -
 CC EMBL; D63942; BAA2617.1; -
 CC EMBL; BC054790; AAH54790.1; -
 CC HSSP; P15116; INCI
 CC MGD; MG1:105057; Cdh5.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR00233; Cadherin_C_term.
 CC Pfam; PF00028; cadherin; 5.
 CC Pfam; PF01049; Cadherin_C_term; 1.
 CC PRINTS; PR00205; CADHERIN.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL. 1 24 POTENTIAL.
 FT PROPEP 25 45 POTENTIAL.
 FT CHAIN 46 784 VASCULAR ENDOTHELIAL-CADHERIN.
 FT TRANSMEM 46 593 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 594 620 POTENTIAL.
 FT DOMAIN 621 784 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 46 149 CADHERIN 1.
 FT DOMAIN 150 256 CADHERIN 2.
 FT DOMAIN 257 371 CADHERIN 3.
 FT DOMAIN 372 476 CADHERIN 4.
 FT DOMAIN 477 593 CADHERIN 5.
 FT DOMAIN 738 753 SER-RICH.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 784 AA; 87902 MW; 7B75698DE2F7E160 CRC64;
 QY Query Match 100.0%; Score 92; DB 1; Length 784;
 QY Best Local Similarity 100.0%; Pred. No. 8.5e-07;
 Db Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 CAD5_PIG STANDARD; PRT; 782 AA.
 ID CAD5_PIG
 AC 002640;
 DT 15-UTR-1998 (Rel. 36, Created)
 DT 15-UTR-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5).
 GN Cdh5.
 OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kishnaw P.J.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions. It
 CC associates with alpha-catenin forming a link to the cytoskeleton
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Found at cell-cell
 CC boundaries and probably at cell-matrix boundaries (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y13919; CAA74225.1; -
 CC HSSP; P09603; IEDH.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR00233; Cadherin_C_term.
 CC Pfam; PF00028; cadherin; 5.
 CC Pfam; PF01049; Cadherin_C_term; 1.
 CC PRINTS; PR00205; CADHERIN.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL. 1 22 POTENTIAL.
 FT PROPEP 23 44 POTENTIAL.
 FT CHAIN 45 782 VASCULAR ENDOTHELIAL-CADHERIN.
 FT TRANSMEM 45 592 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 593 619 POTENTIAL.
 FT DOMAIN 620 782 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 45 148 CADHERIN 1.
 FT DOMAIN 149 255 CADHERIN 2.
 FT DOMAIN 256 370 CADHERIN 3.
 FT DOMAIN 371 475 CADHERIN 4.
 FT DOMAIN 476 592 CADHERIN 5.
 FT DOMAIN 736 751 SER-RICH.
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 782 AA; 87546 MW; 7403F974E2DF782F CRC64;
 QY Query Match 94.6%; Score 87; DB 1; Length 782;
 QY Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Db Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 CAD5_HUMAN STANDARD; PRT; 784 AA.
 ID CAD5_HUMAN
 AC P33151;
 DT 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5)
 DE (7B4 antigen) (CD144 antigen).
 GN CDH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endothelial cells;
 RX MEDLINE=95353875; PubMed=7627717;
 RA Breviaro F., Caveda L., Corada M., Martin-Padura I., Navarro P.,
 RA Golay J., Introna M., Gulino D., Lampugnani M.G., Dejana E.;
 RT "Functional properties of human vascular endothelial cadherin
 (7B4/cadherin-5), an endothelium-specific cadherin.";
 RL Atheroscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97362755; PubMed=9219219;
 RA Ali J., Liao F., Martens E., Muller W.A.;
 RT "Vascular endothelial cadherin (VE-cadherin): cloning and role in
 endothelial cell-cell adhesion.";
 RL Microcirculation 4:267-277(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitejima M., Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent
 heterophilic interactions between different subclasses of type-II
 classic cadherins.";
 RL Biochem. J. 349:159-167(2000).
 RN [4]
 RP SEQUENCE OF 5-784 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins
 in nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 RN [5]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Endothelial cells;
 RX MEDLINE=992394977; PubMed=1522121;
 RA Lampugnani M.G., Resnati M., Raiteri M., Pigott R., Pisacane A.,
 RA Hoven G., Ruco L.P., Dejana E.;
 RT "A novel endothelial-specific membrane protein is a marker of
 cell-cell contacts.";
 RL J. Cell Biol. 118:1511-1522(1992).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions. It
 CC associates with alpha-catenin forming a link to the cytoskeleton.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Found at cell-cell
 CC boundaries and probably at cell-matrix boundaries.
 CC -1- TISSUE SPECIFICITY: Endothelial tissues and brain.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -1- DATABASE: NAME=PROV, NOTE=CD guide CD144 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd144.htm".
 CC -----
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DR EMBL; X79981; CAA56306.1; -;
 DR EMBL; U84722; AAB41796.1; -;
 DR EMBL; AB035304; BAA87418.1; -;
 DR EMBL; X59796; CAA42468.1; -;
 DR PIR; S49893; IJHUC5.
 DR HSSP; P15116; INCU.
 DR GlycoSuiteDB; P31511; -;
 DR Genew; HGNC:1764; CDH5.
 DR MIM; 601120; -;
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF01049; cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL. 1 25
 FT PROPEP 26 47
 FT CHAIN 48 784
 FT DOMAIN 48 593
 FT TRANSMEM 594 620
 FT DOMAIN 621 784
 FT DOMAIN 48 151
 FT DOMAIN 152 258
 FT DOMAIN 259 372
 FT DOMAIN 373 477
 FT DOMAIN 478 593
 FT DOMAIN 593 736
 FT CARBOHYD 61 61
 FT CARBOHYD 112 112
 FT CARBOHYD 157 157
 FT CARBOHYD 362 362
 FT CARBOHYD 442 442
 FT CARBOHYD 523 523
 FT CARBOHYD 535 535
 FT CONFLICT 517 517
 SQ SEQUENCE 784 AA; 87516 MW; F643BFC22A599DE CRC64;
 Query Match 94.6%; Score 87; DB 1; Length 784;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DWIMQMHIDEKN 14
 Db 48 DWIMQMHIDEKN 61
 ID CADU_HUMAN STANDARD; PRT; 772 AA.
 AC Q9H159;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cadherin-19 precursor (UNQ478/PRO941).
 GN CDH19 OR CDH7L2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20453188; PubMed=10995570;
 RX Kools P., Van Imschoot G., van Roy F.;
 RT "Characterization of three novel human cadherin genes (CDH7, CDH19,
 RT and CDH20) clustered on chromosome 18q22-q23 and with high homology
 RT to chicken cadherin-7.";

Genomics 68:283-295 (2000).

-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUE SPECIFICITY: Expressed in many tissues, with the exception of uterus.

-1- SIMILARITY: Contains 5 cadherin domains.

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EMBL; AJ007607; CAC13126.1; -
 DR EMBL; AY358654; AAQ89017.1; -
 DR HSSP; P15116; INCU.
 DR Genew; HGNC:1758; CDH19.
 MIM; 603016; -
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 43 POTENTIAL.
 FT CHAIN 44 772 CADHERIN-19.
 FT DOMAIN 44 596 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 597 617 POTENTIAL.
 FT DOMAIN 618 772 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 149 148 CADHERIN 1.
 FT DOMAIN 257 370 CADHERIN 2.
 FT DOMAIN 371 470 CADHERIN 3.
 FT DOMAIN 470 581 CADHERIN 4.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 772 AA; 87002 MW; 650AD27480343C39 CRC64;

Query Match 56.5%; Score 52; DB 1; Length 772;
 Best Local Similarity 53.8%; Pred. No. 1.6;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WIMNCHIDEKN 14
 DB 45 WVMNQFVPEKN 57

RESULT 5
 CAD8_HUMAN STANDARD; PRT; 799 AA.
 ID CAD8_HUMAN
 AC P55286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cadherin-8 precursor.

GN CDH8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP PubMed=10861224;
 RX Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
 RA "Identification of three human type-II classic cadherins and frequent heterophilic interactions between different subclasses of type-II classic cadherins.";
 RT Biochem. J. 349:159-167 (2000).
 RL [2]
 RN SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of cadherin extracellular domain and provides further evidence for two structurally different types of cadherin.";
 RT Cell Adhes. Commun. 2:15-26 (1994).
 RL [3]
 RN SEQUENCE OF 294-799 FROM N.A.
 RP TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in nervous tissue.";
 RL Cell Regul. 2:261-270 (1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain nerve cell lines, such as retinoblasts, glioma cells and neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.

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EMBL; AB035305; BAA87419.1; -
 EMBL; U34060; AAA55628.1; ALT_INIT.
 DR HSSP; P15116; INCU.
 DR Genew; HGNC:1767; CDH8.
 DR MIM; 603008; -
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.
 FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.

FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 647 647 V -> D (IN REF. 2 AND 3).
 FT CONFLICT 799 AA; 88253 MW; 9B119B86039C6A0A CRC64;
 SQ SEQUENCE

Query Match 53.3%; Score 49; DB 1; Length 799;
 Best Local Similarity 63.6%; Pred. No. 4.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WNNQMHIDE 12
 Db 63 WNNQMFVLEE 73

RESULT 6

CAD8_MOUSE STANDARD; PRT; 799 AA.

ID CAD8_MOUSE STANDARD; PRT; 799 AA.
 AC P97251;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cadherin-8 precursor.
 GN CDH8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=97174321; PubMed=9022055;
 RA Korematsu K., Redies C.;
 RT "Restricted expression of cadherin-8 in segmental and functional
 subdivisions of the embryonic mouse brain.";
 RL Dev. Dyn. 208:178-189(1997).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC -----
 DR EMBL; X95600; CAA64857.1; -
 DR HSSP; P15116; INCU
 DR MGD; MGI:107434; Cdh8.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin_5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KM Signal.
 FT SIGNAL. 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.

FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.
 FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

Query Match 53.3%; Score 49; DB 1; Length 799;
 Best Local Similarity 63.6%; Pred. No. 4.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WNNQMHIDE 12
 Db 63 WNNQMFVLEE 73

RESULT 7

CAD8_RAT STANDARD; PRT; 799 AA.

ID CAD8_RAT STANDARD; PRT; 799 AA.
 AC 054800; 054801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cadherin-8 precursor.
 GN CDH8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RX MEDLINE=98190518; PubMed=9521872;
 RA Kido M., Obata S., Tanihara H., Koehelle J.M., Seldin M.F.,
 RA Taketani S., Suzuki S.T.;
 RT "Molecular properties and chromosomal location of cadherin-8.";
 RL Genomics 48:186-194(1998).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=054800-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=054800-2; Sequence=VSP_000638, VSP_000639;
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC -----
 DR EMBL; AB010436; BAA24452.1; -
 DR EMBL; AB010437; BAA24453.1; -
 DR HSSP; P15116; INCU
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin_5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.


```

CC -!- SIMILARITY: Contains 5 cadherin domains.
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CC -----
CC EMBL; AF055342; AAC33675.1; -.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR002023; Cadherin_C_term.
CC Pfam; PF00028; cadherin; 5.
CC Pfam; PF01049; Cadherin_C_term; 1.
CC SMART; SM00112; CA; 5.
CC DR PROSITE; PS00232; CADHERIN 1; 3.
CC DR PROSITE; PS0268; CADHERIN 2; 5.
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
CC Signal.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT PROPEP 23 53 POTENTIAL.
CC FT CHAIN 54 792 CADHERIN-11.
CC FT DOMAIN 54 613 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 614 634 POTENTIAL.
CC FT DOMAIN 635 792 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 54 159 CADHERIN 1.
CC FT DOMAIN 160 268 CADHERIN 2.
CC FT DOMAIN 269 383 CADHERIN 3.
CC FT DOMAIN 384 486 CADHERIN 4.
CC FT DOMAIN 487 608 CADHERIN 5.
CC FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 792 AA; 87572 MW; 3E3488C686731AB CRC64;

Query Match 48.9%; Score 45; DB 1; Length 792;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 WIMWQMIDEE 12
   |||  ||
Db 55 WVMNQFVIEE 65

RESULT 10
CADB_HUMAN STANDARD; PRT; 796 AA.
ID CADB_HUMAN Q15065; Q15065; Q9U093; Q9U094;
AC P55287; Q15065; Q15065; Q9U093; Q9U094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN CDH11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=9507306; PubMed=7982033;
RA Tanihara H., Sano K., Heimark R.L., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin.";
RL Cell Adhes. Commun. 2:15-26(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Osteosarcoma;
RX MEDLINE=9421632; PubMed=8163513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A.,

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RA Kudo A., Amann E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts.";
RL J. Biol. Chem. 269:12092-12098(1994).
RN [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins
RT in nervous tissue.";
RL Cell Regul. 2:261-270(1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Kools P.F.J., Hogendoorn P.C.W., Bovee J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
RT molecules are detectable in both human cancer and normal cells.";
RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=P55287-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
CC -!- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC other tissues. Expressed in neuroblasts.
CC -!- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L34056; AAA35622.1; -.
CC EMBL; D21254; BAA04798.1; -.
CC EMBL; D21255; BAA04799.1; -.
CC EMBL; AF060370; AAD27755.1; -.
CC EMBL; AF060369; AAD27755.1; JOINED.
CC EMBL; AF060370; AAD27756.1; -.
CC EMBL; AF060369; AAD27756.1; JOINED.
CC PIR; A38992; A38992.
CC HSSP; P15116; INCU.
CC GeneW; HGNC:1750; CDH11.
CC MIM; 600023; -.
CC GO; GO:0016021; C:Integral to membrane; NAS.
CC GO; GO:0077156; P:homophilic cell adhesion; NAS.
CC GO; GO:0001503; P:ossification; NAS.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR002023; Cadherin_C_term.
CC Pfam; PF00028; cadherin; 5.
CC Pfam; PF01049; Cadherin_C_term; 1.
CC PRINTS; PR00205; CADHERIN.
CC SMART; SM00112; CA; 5.
CC PROSITE; PS00232; CADHERIN 1; 3.
CC PROSITE; PS0268; CADHERIN 2; 5.
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
CC Signal; Alternative splicing.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT PROPEP 23 53 POTENTIAL.
CC FT CHAIN 54 796 CADHERIN-11.
CC FT DOMAIN 54 617 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 618 640 POTENTIAL.
CC FT DOMAIN 641 796 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 54 159 CADHERIN 1.
CC FT DOMAIN 160 268 CADHERIN 2.

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FT DOMAIN 269 383 CADHERIN 3.
 FT DOMAIN 384 486 CADHERIN 4.
 FT CAROXYD 487 612 CADHERIN 5.
 FT CAROXYD 485 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROXYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 632 693 VIVLFVTRPKEPKEPLVEEDVEDVITYDDGSGERD
 TEADRTADNPDCINGFIFR -> GCPSPMEPRSDMR
 LTLTGFLMSPSYKXNRRCILGVKIKPLVYVATESPT
 LITSL (in isoform 2).
 /FRTID=VSP_000640.
 Missing (in isoform 2).
 /FRTID=VSP_000641.
 FT VARSPLIC 694 796 RL -> SV TIN REF. 2).
 FT CONFLICT 271 272 M -> I (IN REF. 2).
 FT CONFLICT 273 273 E -> K (IN REF. 2).
 FT CONFLICT 340 340 S -> A (IN REF. 2).
 FT CONFLICT 373 373 Q -> K (IN REF. 2).
 FT CONFLICT 471 471
 SO SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB82E CRC64;

Query Match 48.9%; Score 45; DB 1; Length 796;
 Best Local Similarity 54.5%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WINNOMHIDE 12
 DB 55 WANNOFFVIBE 65

RESULT 11
 CABD_MOUSE
 AC P55286; STANDARD; PRT; 796 AA.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 OS CH11 OR CABD-11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269886; PubMed=7750649;
 RA Hofmann I.H., Balling K.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 cadherin";
 RL Dev. Biol. 169:337-346(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 in the head, somite, and limb bud of early mouse embryos";
 RL Dev. Biol. 169:347-358(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amano E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
 RA Bosak S.A., Morley P.J., McKernan K.J., Maller J.A., Guaratne P.H.,
 RA Richards S., Wootley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP DEVELOPMENTAL STAGE.
 RX STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=879495;
 RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 fetal, immature, and adult mice utilizing the polymerase chain
 reaction";
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.

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 CC -----

DR EMBL; X77557; CA54674.1; -
 DR EMBL; D31963; BAA06730.1; -
 DR EMBL; D21253; BAA04797.1; -
 DR EMBL; BC046314; AAH46314.1; -
 DR PIR; A53584; A53584.
 DR PIR; I48277; I48277.
 DR PIR; I49556; I49556.
 DR HSSP; P15116; INCU.
 DR MGD; MGI:99217; Cdhl1.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KM Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;

FT SIGNAL 1 24
 FT PROPEP 25 53
 FT CHAIN 54 796
 FT DOMAIN 54 617
 FT TRANSMEM 618 640
 FT DOMAIN 641 796
 POTENTIAL.
 POTENTIAL.
 CADHERIN-11.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 54 159 CADHERIN 1.
FT DOMAIN 160 268 CADHERIN 2.
FT DOMAIN 269 383 CADHERIN 3.
FT DOMAIN 384 486 CADHERIN 4.
FT DOMAIN 487 612 CADHERIN 5.
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 462 462 E -> D (IN REF. 1).
FT CONFLICT 589 589 T -> L (IN REF. 2).
FT CONFLICT 655 655 D -> N (IN REF. 2).
FT CONFLICT 751 751 V -> M (IN REF. 1).
FT CONFLICT 777 777 P -> Q (IN REF. 2).
FT CONFLICT 782 782 L -> P (IN REF. 2).
SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641D529 CRC64;

Query Match 48.9%; Score 45; DB 1; Length 796;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 WIMNQMIDEE 12
Db 55 WVMNQFVVEE 65

RESULT 12
CADM_MOUSE STANDARD; PRT; 813 AA.
ID CADM_MOUSE
AC Q9WT5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-22 precursor (PB-cadherin).
GN CDH22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND DEVELOPMENTAL STAGE.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=99326347; PubMed=10398531;
RA Kitajima K., Koshimizu U., Nakamura T.;
RT "Expression of a novel type of classic cadherin, PB-cadherin in
RT developing brain and limb buds.";
RL Dev. Dyn. 215:206-214(1999).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. PB-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain. Abundant in
CC olfactory bulb, cerebrum, and cerebellum, less in pons, medulla,
CC and spinal cord. Low expression in heart. No expression in lung,
CC liver, spleen, kidney, testis, stomach, intestine, colon, and
CC placenta.
CC -1- DEVELOPMENTAL STAGE: Expressed at 9.5 dpc onwards. At 10.5 dpc, in
CC brain (telencephalic vesicles and isthmus), spinal cord and limb
CC buds (in the zone of polarizing activity). At 14.5 dpc, in
CC olfactory bulb and cerebellum.
CC -1- INDUCTION: Down-regulated by thyroid hormone.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB019618; BAA34426.1; -

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DR MGD; MGI:1341843; Cdh22.
DR HSSP; P15116; INCU.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; cadherin; 5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN 1; 2.
DR PROSITE; PS00268; CADHERIN 2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 813 CADHERIN-22.
FT DOMAIN 33 621 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 622 642 POTENTIAL.
FT DOMAIN 643 813 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 61 165 CADHERIN 1.
FT DOMAIN 166 274 CADHERIN 2.
FT DOMAIN 275 391 CADHERIN 3.
FT DOMAIN 392 495 CADHERIN 4.
FT DOMAIN 496 613 CADHERIN 5.
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 813 AA; 88021 MW; 5510F9848D976567 CRC64;

Query Match 48.9%; Score 45; DB 1; Length 813;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 WIMNQMIDEE 12
Db 61 WVMNQFVVEE 71

RESULT 13
CADM_RAT STANDARD; PRT; 813 AA.
ID CADM_RAT
AC Q63315; Q63561;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-22 precursor (PB-cadherin).
GN CDH22.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
RC STRAIN=Wistar; TISSUE=Brain; and Pituitary;
RX MEDLINE=96212232; PubMed=9626716;
RA Sugimoto K., Honda S., Yamamoto T., Ueki T., Monden M., Kaji A.,
RA Matsumoto K., Nakamura T.;
RT "Molecular cloning and characterization of a newly identified member
RT of the cadherin family, PB-cadherin.";
RL J. Biol. Chem. 271:11548-11556(1996).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. PB-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=Q63315-1; Sequence=Displayed;
CC IsoId=Q63315-2; Sequence=VSP_000643; VSP_000644;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Strongly expressed in the pituitary gland and

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the brain (in the inner granular and glomerular layers of the olfactory bulb, anterior olfactory nucleus, primary olfactory cortex, Purkinje cell layer of cerebellum, and pineal gland). Low expression in lung and heart. No expression in submandibular gland, thymus, liver, spleen, adrenal, and kidney.

CC -1- DEVELOPMENTAL STAGE: Expressed strongly in fetal brain.

CC -1- SIMILARITY: Contains 5 cadherin domains.

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CC EMBL: D83348; BAA11894.1; -.

CC EMBL: D83349; BAA11895.1; -.

CC HSSP: P15116; INCU.

CC InterPro: IPR002126; Cadherin.

CC InterPro: IPR000233; Cadherin_C_term.

CC Pfam: PF00028; Cadherin_5.

CC Pfam: PF01049; Cadherin_C_term; 1.

CC PRINTS: PR00205; CADHERIN.

CC SMART: SMO0112; CA: 5.

CC PROSITE: PS00232; CADHERIN_1; 2.

CC PROSITE: PS50268; CADHERIN_2; 5.

CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal; Alternative splicing.

CC SIGNAL: 1 33

CC CHAIN: 34 813

CC DOMAIN: 33 621

CC TRANSMEM: 622 642

CC DOMAIN: 643 813

CC DOMAIN: 61 165

CC DOMAIN: 166 274

CC DOMAIN: 275 391

CC DOMAIN: 392 495

CC DOMAIN: 496 613

CC CARBOHYD: 159 159

CC CARBOHYD: 463 463

CC CARBOHYD: 609 609

CC VARSPLIC: 668 694

CC FT: 695 813

CC FT: VARSPLIC

CC FT: MISSING (in isoform 2).

CC FT: /FTid=VSP_000644.

CC FT: /FTid=VSP_000644.

CC FT: 30BEA60B5DD2D467B CRC64;

CC FT: 813 AA; 87978 MW; 30BEA60B5DD2D467B CRC64;

CC FT: SEQUENCE

CC FT: 48.9%; Score 45; DB 1; Length 813;

CC FT: Best Local Similarity 54.5%; Pred. No. 21;

CC FT: Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CC FT: 2 WIMWQHIDEI 12

CC FT: 61 WVMNQFVEE 71

CC FT: ID CADO HUMAN STANDARD; FRT; 819 AA.

CC FT: AC Q86UP0; Q86UP1; Q9NT84;

CC FT: DT 15-MAR-2004 (Rel. 43, Last sequence update)

CC FT: DT 15-MAR-2004 (Rel. 43, Last annotation update)

CC FT: DE Cadherin-24 precursor (UNC2834/PRO34009).

CC FT: GN CDH24 OR CDH11.

CC FT: OS Homo sapiens (Human).

CC FT: OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC FT: OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

CC FT: OC NCBI_taxid=9606;

CC FT: RN [1]

CC FT: SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH

CATENINS.

RX MEDLINE-22753805; PubMed=12734196;

RA Katsifas B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;

RT "Characterization of cadherin-24, a novel alternatively spliced type II cadherin.";

RL J. Biol. Chem. 278:27513-27519 (2003).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE-22887296; PubMed=12975309;

RA Clark H.F., Gunney A.V., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshgiri S., Simons L., Singh V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;

RA "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RA Blum H., Bauerach S., Mewes H.-W., Gassenhuber J., Wiemann S.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. Cadherin-24 mediate strong cell-cell adhesion.

CC -1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1; Synonyms=Long form;

CC IsoId=Q86UP0-1; Sequence=Displayed;

CC Name=2; Synonyms=Short form;

CC IsoId=Q86UP0-2; Sequence=VSP_008717;

CC Name=3;

CC IsoId=Q86UP0-3; Sequence=VSP_008718, VSP_008719;

CC Note=No experimental confirmation available;

CC -1- SIMILARITY: Contains 5 cadherin domains.

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CC EMBL: AY260900; AAP20590.1; -.

CC EMBL: AY260901; AAP20591.1; -.

CC EMBL: AY358199; AAQ88566.1; -.

CC EMBL: AL137477; CAB70758.1; -.

CC PIR: T46418; T46418.

CC Gene: HGNC:14265; CDH24.

CC InterPro: IPR002126; Cadherin.

CC InterPro: IPR000233; Cadherin_C_term.

CC Pfam: PF00028; Cadherin_5.

CC Pfam: PF01049; Cadherin_C_term; 1.

CC PRINTS: PR00205; CADHERIN.

CC SMART: SMO0112; CA: 4

CC PROSITE: PS00232; CADHERIN_1; 2.

CC PROSITE: PS50268; CADHERIN_2; 5.

CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal; Multigene family; Alternative splicing.

CC SIGNAL: 1 19

CC PROPEP: 21 44

CC CHAIN: 45 819

CC DOMAIN: 45 641

CC FT: EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 642 662 POTENTIAL.
FT DOMAIN 663 819 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 46 150 CADHERIN 1.
FT DOMAIN 151 259 CADHERIN 2.
FT DOMAIN 260 374 CADHERIN 3.
FT DOMAIN 375 517 CADHERIN 4.
FT DOMAIN 517 630 CADHERIN 5.
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 455 492 Missing (in isoform 2).
FT VARSPLIC 1 427 /FTID=VSP_008719.
FT VARSPLIC 428 492 Missing (in isoform 3).
FT VARSPLIC 428 492 /FTID=VSP_008718.
FT VARSPLIC 428 492 ECTHPTAFLDREARAHMNLTVLATLGMWGPERGVPVLL
FT VARSPLIC 428 492 VAEMGAPAPAPORSPGSAVGIPQ -> MNIVCTWCSHS
FT VARSPLIC 428 492 ATLSTCTHAYFMGCLMCLVASCIGHAHPMLRVNCVVC
FT VARSPLIC 428 492 VWRVCFGVIPS (in isoform 3).
FT VARSPLIC 428 492 /FTID=VSP_008719.
SQ SEQUENCE 819 AA; 87751 MW; 9083034FF18A7E4A CRC64;

Query Match 48.9%; Score 45; DB 1; Length 819;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 WYWNQMHIDE 12
Db 46 WYWNQFVIEE 56

RESULT 15
CADM HUMAN STANDARD; PRT; 828 AA.
ID Q9U99; 043205;
AC Q9U99; 043205;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-22 precursor.
GN CDH22 OR C20ORF25.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailely O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.B., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaesajaho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McCormachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.U.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Thorpe A.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Whiting L., Wray P.W., Hubbard T., Dubin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).

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RN [2]
RP SEQUENCE OF 449-828 FROM N.A.
RC TISSUE=Brain;
RA Yu W., Sargison J., Gibbs R.A.;
RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. PB-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL031687; CAB51587.2; -
DR EMBL; AF035300; AAB8183.1; -
DR Genew; HGNC:13251; CDH22.
DR HSSP; P15116; INCU.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR002333; Cadherin_C_term.
DR Pfam; PF00028; cadherin; 5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS0268; CADHERIN_2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 828 CADHERIN-22.
FT DOMAIN 36 624 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 625 645 POTENTIAL.
FT DOMAIN 646 828 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 64 CADHERIN 1.
FT DOMAIN 169 277 CADHERIN 2.
FT DOMAIN 278 394 CADHERIN 3.
FT DOMAIN 395 498 CADHERIN 4.
FT DOMAIN 499 616 CADHERIN 5.
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 828 AA; 89091 MW; 520F7B1D1F624DCA CRC64;

Query Match 48.9%; Score 45; DB 1; Length 828;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 WYWNQMHIDE 12
Db 64 WYWNQFVIEE 74

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Search completed: July 29, 2004, 11:35:22
 Job time : 6.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:30:55 ; Search time 31 Seconds
(without alignments)
152.670 Million cell updates/sec

Title: US-10-040-128-3
Perfect score: 92
Sequence: 1 DMINQMHIDEKNT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	87	94.6	782	6	Q8NMW5	Q8NMW5 sus. scrofa
2	64	69.6	773	13	Q8AYD0	Q8AYD0 gallus galli
3	49	53.3	247	11	Q8C9N7	Q8C9N7 mus musculus
4	49	53.3	716	11	Q8C449	Q8C449 mus musculus
5	49	53.3	716	11	Q8C375	Q8C375 mus musculus
6	49	53.3	754	11	Q8BRK4	Q8BRK4 mus musculus
7	48	52.2	524	5	001321	001321 caenorhabdi
8	46	50.0	313	16	Q88HL3	Q88HL3 pseudomonas
9	45	48.9	176	10	Q8RYF1	Q8RYF1 avena strig
10	45	48.9	241	4	Q86TS8	Q86TS8 homo sapien
11	45	48.9	310	10	Q8W5G3	Q8W5G3 oryza sativ
12	45	48.9	333	2	Q9L3G9	Q9L3G9 erwilia rha
13	45	48.9	350	3	Q00870	Q00870 neectria hae
14	45	48.9	493	4	Q96L07	Q96L07 homo sapien
15	45	48.9	566	3	Q9CA77	Q9CA77 cladosporiu
16	45	48.9	781	4	Q86UP1	Q86UP1 homo sapien

17	45	48.9	794	13	Q93264	Q93264 xenopus lae
18	45	48.9	796	4	Q96C29	Q96C29 homo sapien
19	45	48.9	796	11	Q8C7Q6	Q8C7Q6 mus musculus
20	45	48.9	819	4	Q86UP0	Q86UP0 homo sapien
21	45	48.9	839	5	Q9N2R2	Q9N2R2 strongyloce
22	44.5	48.4	963	10	Q9STU7	Q9STU7 arabidopsis
23	44	47.8	76	11	Q8BLT5	Q8BLT5 mus musculus
24	44	47.8	219	16	Q8BCK3	Q8BCK3 shewanella
25	44	47.8	271	5	Q8T9K7	Q8T9K7 drosophila
26	44	47.8	271	5	Q9VLX9	Q9VLX9 drosophila
27	44	47.8	337	11	Q8BLB5	Q8BLB5 mus musculus
28	44	47.8	340	11	Q8BLT4	Q8BLT4 mus musculus
29	44	47.8	500	16	Q9PT97	Q9PT97 straphylococ
30	44	47.8	500	16	Q8NMW1	Q8NMW1 straphylococ
31	44	47.8	551	13	Q8AMW2	Q8AMW2 gallus galli
32	44	47.8	630	4	Q81Y78	Q81Y78 homo sapien
33	44	47.8	785	11	Q8BMW2	Q8BMW2 mus musculus
34	44	47.8	790	4	Q8N522	Q8N522 homo sapien
35	44	47.8	790	13	Q91838	Q91838 xenopus lae
36	44	47.8	794	4	Q86UD2	Q86UD2 homo sapien
37	44	47.8	798	13	Q8QGH3	Q8QGH3 gallus galli
38	44	47.8	798	13	Q7ZYV7	Q7ZYV7 gallus galli
39	44	47.8	801	11	Q9Z0M3	Q9Z0M3 mus musculus
40	44	47.8	1356	5	Q81CG0	Q81CG0 plasmodium
41	44	47.8	1497	16	Q87G80	Q87G80 vibrio para
42	43	46.7	192	16	Q7VD46	Q7VD46 prochloroco
43	43	46.7	246	16	Q7VZB4	Q7VZB4 prochloroco
44	43	46.7	248	16	Q7VA66	Q7VA66 prochloroco
45	43	46.7	253	16	Q7U5H3	Q7U5H3 synechococc

ALIGNMENTS

RESULT 1
Q8NMW5 PRELIMINARY; PRT; 782 AA.
AC Q8NMW5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE VE cadherin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirano M., Hirano K., Nishimura J., Kanade H.;
RT "Transcriptional up-regulation of p27kip1 during contact-induced
RT growth arrest in the endothelial cells.",
RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99119339; PubMed=9918866;
RA Hirano M., Nitro N., Hirano K., Nishimura J., Hartshorne D.J.,
RA Kanade H.;
RT "Expression, subcellular localization and cloning of the 130 kDa
RT regulatory subunit of myosin phosphatase in porcine aortic endothelial
RT cells.",
RL Biochem. Biophys. Res. Commun. 254:490-496 (1999).
CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
CC THEY DIFFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
CC SORTING OF HETEROGENEOUS CELL TYPES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AB046120; BAB82983.1; -;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0005194; F:cell adhesion molecule activity; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.

```

OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs."
DR Nature 420:563-573(2002).
DR EMBL: AK041728; BAC31041.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR Pfam: PF00028; cadherin; 5.
DR PRINTS: PR00205; CADHERIN_2.
DR SMART: SMO0112; CA; 1.
DR PROSITE: PS00232; CADHERIN_1; 1.
DR PROSITE: PS50268; CADHERIN_2; 2.
SQ SEQUENCE 247 AA; 27565 MW; DF7551A97A29289D CRC64;

Query Match 53.3%; SCORE 49; DB 11; Length 247;
Best Local Similarity 63.6%; Pred. No. 5.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 WINNOMHIDE 12
DB 63 WINNOMFYLEE 73
ID 08C449 PRELIMINARY; PRT; 716 AA.
AC 08C449;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cadherin 8.
GN CDH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs."
DR Nature 420:563-573(2002).
DR EMBL: AK083092; BAC38758.1; -.
DR MGI: MGI:107434; Cdh8.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR00233; Cadherin_C_term.
DR Pfam: PF00028; cadherin; 5.
DR Pfam: PF01049; cadherin_C_term; 1.
DR PRINTS: PR00205; CADHERIN_
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 53.3%; SCORE 49; DB 11; Length 716;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 WINNOMHIDE 12

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Db      63 WWMNQMFVLEE 73

RESULT 5
Q8C375      PRELIMINARY;      PRT;      716 AA.
AC      Q8C375;
DT      01-MAR-2003 (TEMBLrel. 23, Created)
DT      01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE      Cadherin 8.
GN      CDH8.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      NCB1_TaxID=10090;
RC      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6J; TISSUE=Head;
RA      MEDLINE=22354683; PubMed=12466851;
RT      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
DR      EMBL; AK086711; BAC39724.1; -.
DR      MGD; MGI:107434; Cdh8.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005509; F:calcium ion binding; IEA.
DR      GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR      InterPro; IPR002126; Cadherin.
DR      InterPro; IPR000233; Cadherin_C_term.
DR      Pfam; PF00028; cadherin; 5.
DR      Pfam; PF01049; Cadherin_C_term; 1.
DR      PRINTS; PR00205; CADHERIN.
DR      SMART; SM00112; CA; 5.
DR      PROSITE; PS00232; CADHERIN_1; 3.
DR      PROSITE; PS50268; CADHERIN_2; 5.
DR      PROSITE; PS50268; CADHERIN_2; 5.
SQ      SEQUENCE 716 AA; 79149 MW; 5BD598F638624A CRC64;

Query Match      53.3%; Score 49; DB 11; Length 716;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 WWMNQMHIDE 12
Db      63 WWMNQMFVLEE 73

RESULT 6
Q8BRK4      PRELIMINARY;      PRT;      754 AA.
AC      Q8BRK4;
DT      01-MAR-2003 (TEMBLrel. 23, Created)
DT      01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE      Cadherin 8.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      NCB1_TaxID=10090;
RC      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6J; TISSUE=Cortex;
RA      MEDLINE=22354683; PubMed=12466851;
RT      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
DR      EMBL; AK04046; BAC31751.1; -.
DR      EMBL; AK04046; BAC31751.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
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DR      GO; GO:0005509; F:calcium ion binding; IEA.
DR      GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR      InterPro; IPR002126; Cadherin.
DR      InterPro; IPR000233; Cadherin_C_term.
DR      Pfam; PF00028; cadherin; 5.
DR      Pfam; PF01049; Cadherin_C_term; 1.
DR      PRINTS; PR00205; CADHERIN.
DR      SMART; SM00112; CA; 5.
DR      PROSITE; PS00232; CADHERIN_1; 3.
DR      PROSITE; PS50268; CADHERIN_2; 5.
DR      PROSITE; PS50268; CADHERIN_2; 5.
SQ      SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;

Query Match      53.3%; Score 49; DB 11; Length 754;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 WWMNQMHIDE 12
Db      63 WWMNQMFVLEE 73

RESULT 7
001321      PRELIMINARY;      PRT;      524 AA.
AC      001321; P91858;
DT      01-JUL-1997 (TEMBLrel. 04, Created)
DT      01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT      01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE      P26H9.1 protein.
GN      P26H9.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OX      Rhabditidae; Pelodertinae; Caenorhabditis.
RN      [1]
RP      NCB1_TaxID=6239;
RC      SEQUENCE FROM N.A.
RA      Baynes C.;
RL      Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94150718; PubMed=7906398;
RA      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA      Boulfield J., Burton V., Connell M., Copsey T., Cooper J., Coulson A.,
RA      Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA      Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA      Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA      Parsons V., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,
RA      Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA      Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA      Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT      "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT      elegans.";
RL      Nature 368:32-38(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Sims M.;
RL      Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; Z61516; CAB04206.1; -.
DR      EMBL; Z75535; CAB04206.1; JOINED.
DR      EMBL; Z75535; CAB99829.1; -.
DR      EMBL; Z81516; CAA99829.1; JOINED.
DR      PIR; T20872; T20872.
DR      WormPep; F26H9.1; CE09706.
DR      InterPro; IPR008945; Skp1_Skp2.
SQ      SEQUENCE 524 AA; 60462 MW; 6A85B0C0DCDD2B76 CRC64;

Query Match      52.2%; Score 48; DB 5; Length 524;
Best Local Similarity 53.8%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 WWMNQMHIDEKN 14
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Db 486 WDMHQRNIDEHRN 498

RESULT 8

Q88HL3 PRELIMINARY; PRT; 313 AA.

AC Q88HL3; 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Nickel ABC transporter, permease protein.

GN NICK OR PP343.

OS Pseudomonas putida (strain KT2440).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=160488;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22423060; PubMed=12534463;

RA Nelson K.E., Meinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Bauman M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Kouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazed A., Utecherback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stepanic D., Hobeisel J., Straetz M., Helm S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tsemmler B., Fraser C.M.;

RA "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."

RT EMBL; Microbiol. 4:799-808(2002).

RL EMBL; AB016786; AAN68947.1; -.

DR TIGR; PP3343; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; P:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF00528; BPD_transp; 1.

KW Complete proteome.

SQ SEQUENCE 313 AA; 34571 MW; 0480D2B8523F87C CRC64;

QY 2 WDMHQRNIDEHRN 10

Db 71 WDMHQRNIDEHRN 79

RESULT 9

Q88YFL PRELIMINARY; PRT; 176 AA.

AC Q88YFL; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Putative resistance protein (Fragment).

GN RGA.

OS Avena strigosa (black oat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;

OC Avenae; Avena.

OX NCBI_TaxID=38783;

RN [1]

RP SEQUENCE FROM N.A.

RA Loarce Y., Irigoyen M.L., Fominaya A., Ferrer E.; "Resistance gene analogous in Avena strigosa."

RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AJ437574; CAD26862.1; -.

DE EMBL; AJ437574; CAD26862.1; -.

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR InterPro; IPR002182; NB-ARC.

DR Pfam; PF00931; NB-ARC; 1.

FT NON_TER 1

FT NON_TER 176

SQ SEQUENCE 176 AA; 20133 MW; D60982A15C6FE2F6 CRC64;

Query Match

Best Local Similarity 48.9%; Score 45; DB 10; Length 176;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 WDMHQRNIDEHRN 14

Db 62 WDMHQRNIDEHRN 73

RESULT 10

Q86TS8 PRELIMINARY; PRT; 241 AA.

AC Q86TS8; 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Human full-length cDNA 5-PRIME end of clone CSDB0107P19 of placenta of Homo sapiens (Human).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Genoscope;

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Li W.B., Gruber C., Jesse J., Polayes D.; "Full-length cDNA libraries and normalization."

RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; BX248750; CAD66557.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005509; P:calcium ion binding; IEA.

DR GO; GO:0007156; P:homophilic cell adhesion; IEA.

DR InterPro; IPR002126; Cadherin.

DR Pfam; PF00028; cadherin; 2.

DR PRINTS; PR00205; CADHERIN.

DR SMART; SM00112; CA; 2.

DR PROSITE; PS00232; CADHERIN_1; 1.

DR PROSITE; PS50268; CADHERIN_2; 2.

KW Plasmid.

FT NON_TER 241

SQ SEQUENCE 241 AA; 26348 MW; 4649831B55424604 CRC64;

QY 2 WDMHQRNIDEHRN 12

Db 46 WDMHQRNIDEHRN 56

RESULT 11

Q8W5G3 PRELIMINARY; PRT; 310 AA.

AC Q8W5G3; 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Putative transcription factor.

GN OSJBA0002324.23.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriharoidae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Teitelin T., Riggs P., Hsiao J., Zismann V., Blunt S., Pal G.,
RA Vanaken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUBa0002124 genomic sequence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
DR EMBL: AC090713; AAL34136.1; -.
DR Gramene; Q8W5G3; -.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PSS0868; HLH_2; 1.
SQ SEQUENCE 310 AA; 34267 MW; FCB99DA910830A1D CRC64;

Query Match 48.9%; Score 45; DB 10; Length 310;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DWINQMHIDEKN 14
Db 4 DWIERRRREERYN 17

RESULT 12
Q9L3G9 PRELIMINARY; PRT; 333 AA.
AC Q9L3G9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Endoglucanase precursor (EC 3.2.1.4).
GN CELA.
OS Erwinia rhapontici.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Erwinia.
OX NCBI_TaxID=55212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCPB2989;
RA Saarihati H.T.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NCPB2989;
RA Riecki R.;
RT "Members of the amylovora group of Erwinia are cellulolytic and
RT possess genes homologous to the type II secretion pathway.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276358; CAB89803.1; -.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002037; Glyco_hydro_8.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF01270; Glyco_hydro_8; 1.
DR PRINTS; PR00735; GLHYDRASE8.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1
FT CHAIN 24 333 POTENTIAL. ENDOGLUCANASE.
SQ SEQUENCE 333 AA; 37784 MW; D75CFR21302673A CRC64;

Query Match 48.9%; Score 45; DB 2; Length 333;
Best Local Similarity 46.2%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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QY 2 DWINQMHIDEKN 14
Db 75 WAWTQTHLSNPKN 87

RESULT 13
Q00870 PRELIMINARY; PRT; 350 AA.
AC Q00870;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Kievitone hydrolase precursor.
GN KHS.
OS Nectria haematococca.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=140110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FBI-S; TISSUE=Mycelium;
RX MEDLINE=95383711; PubMed=7655061;
RA Li D., Chung K.R., Smith D.A., Schardl C.L.;
RT "The Fusarium solani gene encoding Kievitone hydrolase, a secreted
RT enzyme that catalyzes detoxification of a bean phytoalexin.";
RL Mol. Plant Microbe Interact. 8:388-397 (1995).
DR EMBL; U39639; AAA87627.1; -.
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 350 KIEVITONE HYDROLASE.
SQ SEQUENCE 350 AA; 38970 MW; CE09B07A7B34C91B CRC64;

Query Match 48.9%; Score 45; DB 3; Length 350;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DWINQMHIDE 11
Db 219 NWTWFQMHPE 229

RESULT 14
Q96LQ7 PRELIMINARY; PRT; 493 AA.
AC Q96LQ7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Nimomiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057922; BAB71613.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin_4.
DR PRINTS; PR00205; CADHERIN.

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DR SMART; SM00112; CA; 4
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 KW Hypothetical protein; Calcium; Calcium-binding; Cell adhesion;
 KW Glycoprotein.
 SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;

Query Match 48.9%; Score 45; DB 4; Length 493;
 Best Local Similarity 54.5%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 MWNMWHIDEE 12
 ||:||||: ||
 Db 46 MWNMWHIDEE 56

RESULT 15

O9C477 PRELIMINARY; PRT; 566 AA.
 AC O9C477;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CATI catalase (EC 1.11.1.6).
 GN CAT-1.
 OS Cladosporium fulvum (Fulvia fulva).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetochytriomycetes incertae sedis;
 OC Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cladosporium.
 OX NCBI TaxID=5499;
 RN [1]
 RP SOURCE FROM N.A.
 RC STRAIN=Race 4;
 RX MEDLINE=20570112; PubMed=11121097;
 RA Bussink H.-J.;
 RT "Identification of two highly divergent catalase genes in the fungal
 tomato pathogen, Cladosporium fulvum.";
 RL Eur. J. Biochem. 268:15-24(2001).
 CC -1- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
 SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
 PEROXIDE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
 CC EMBL; AF222055; AAC53518.1; -.
 DR HSSP; P04040; 1F4J.
 DR GO; GO:0004096; F:catalase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006979; P:response to oxidative stress; IEA.
 DR InterPro: IPR002226; Catalase.
 DR Pfam; PF00199; catalase; 1.
 DR PRINTS; PR00067; CATALASE.
 DR PRODOM; PD000510; Catalase; 1.
 DR PROSITE; PS00437; CATALASE_1; 1.
 DR PROSITE; PS00438; CATALASE_2; 1.
 KW Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
 SQ SEQUENCE 566 AA; 63896 MW; 59023AA3FEFF32334 CRC64;

Query Match 48.9%; Score 45; DB 3; Length 566;
 Best Local Similarity 40.0%; Pred. No. 61;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 DWNMWHIDEEKNT 15
 ||:||||: ||
 Db 238 DWNMWHIDEEKNT 252

Search completed: July 29, 2004, 11:37:09
 Job time : 31 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:30:30 ; Search time 6.6667 Seconds

(without alignments)
117.158 Million cell updates/sec

Title: US-10-040-128-3

Perfect score: 92

Sequence: 1 DWMQMHTDEKNT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	92	100.0	784	1	CAD5_HUMAN P33151 homo sapien
2	87	94.6	782	1	CAD5_PIG O02840 sus scrofa
3	87	94.6	784	1	CAD5_MOUSE P55284 mus musculu
4	57	62.0	772	1	CAD7_HUMAN Q9H159 homo sapien
5	49	53.3	799	1	CAD8_HUMAN P55286 homo sapien
6	49	53.3	799	1	CAD8_MOUSE P97291 mus musculu
7	49	53.3	799	1	CAD8_RAT O54800 gallus norv
8	45	48.9	792	1	CAD8_CHICK O93319 gallus gall
9	45	48.9	796	1	CAD8_HUMAN P55287 homo sapien
10	45	48.9	796	1	CAD8_MOUSE P55288 mus musculu
11	45	48.9	813	1	CAD6_MOUSE Q9WTP5 mus musculu
12	45	48.9	813	1	CAD6_RAT O63315 rattus norv
13	45	48.9	819	1	CAD0_HUMAN O86up0 homo sapien
14	45	48.9	828	1	CAD0_HUMAN Q9u199 homo sapien
15	44	47.8	785	1	CAD7_CHICK Q90763 gallus gall
16	44	47.8	785	1	CAD7_HUMAN Q9u1b5 homo sapien
17	44	47.8	790	1	CAD7_HUMAN Q13634 homo sapien
18	44	47.8	794	1	CAD0_HUMAN P55289 homo sapien
19	44	47.8	801	1	CAD6_HUMAN Q9ubt6 homo sapien
20	43	46.7	435	1	HISX_BUCAL P57201 buchnera ap
21	42.5	46.2	388	1	YUBA_BACSU O32086 bacillus su
22	42	45.7	427	1	CISY_SALTU O68883 salmoneila
23	42	45.7	583	1	GUS2_CAEEL Q93650 caenorhabdi
24	41.3	45.1	392	1	OYEB_SCHPO Q09671 schizosach
25	41	44.6	314	1	NIXB_ECOLI P33591 escherichia
26	41	44.6	768	1	TRPG_ASPAM P18483 aspergillus
27	41	44.6	788	1	CADA_HUMAN O94688 homo sapien
28	41	44.6	789	1	CAD6_RAT P52280 rattus norv
29	41	44.6	789	1	CAD7_HUMAN Q9u1b4 homo sapien
30	41	44.6	789	1	CAD7_HUMAN Q9u1b4 homo sapien
31	41	44.6	790	1	CAD6_CHICK Q90762 gallus gall
32	41	44.6	790	1	P55285 homo sapien
33	40.5	44.0	44	1	OP01_OPICA P83313 opisthophtha

34	40.5	44.0	44	1	OP02_OPICA P83314 opisthophtha
35	40.5	44.0	757	1	IKKX_MOUSE O88351 mus musculu
36	40.5	44.0	757	1	IKKX_RAT Q9qy78 rattus norv
37	40	43.5	146	1	HBBC_HOPLI P82316 hoplosternu
38	40	43.5	200	1	LEUD_HAEIN P44438 haemophilus
39	40	43.5	373	1	LYSI_YEAST P38998 saccharomyc
40	40	43.5	433	1	UROK_MOUSE P06869 mus musculu
41	40	43.5	475	1	PEM2_ARATH Q94480 arabidopsis
42	40	43.5	508	1	TNSD_ECOLI P13921 escherichia
43	40	43.5	518	1	NIRK_THIFE P15052 thiodacillu
44	40	43.5	1742	1	GUNA_CALSA P22534 caldocellum
45	40	43.5	1812	1	SUIS_SUNMU O62653 suncus muri

ALIGNMENTS

RESULT 1
CAD5_HUMAN STANDARD; PRT; 784 AA.
AC P33151;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5)
DE (784 antigen) (CD144 antigen).
GN CDH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=95353875; PubMed=7627717;
RA Breviario F., Cavada L., Corada M., Martin-Padura I., Navarro P.,
RA Goley J., Introna M., Gullino D., Lampugnani M.G., Dejana F.;
RT "Functional properties of human vascular endothelial cadherin
(784/cadherin-5), an endothelium-specific cadherin.";
RT Arterioscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=97362755; PubMed=9219219;
RA Ali J., Liao F., Martens B., Muller W.A.;
RT "Vascular endothelial cadherin (VE-cadherin): cloning and role in
endothelial cell-cell adhesion.";
RT Microcirculation 4:267-277(1997).
RL [3]
RN SEQUENCE FROM N.A.
RP PubMed=10861224;
RX Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
RA "Identification of three human type-II classic cadherins and frequent
heterophilic interactions between different subclasses of type-II
classic cadherins.";
RT Biochem. J. 349:159-167(2000).
RL [4]
RN SEQUENCE OF 5-784 FROM N.A.
RP TISSUE=Brain.
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins
in nervous tissue.";
RT Cell Regul. 2:261-270(1991).
RN [5]
RP PARTIAL SEQUENCE.
RC TISSUE=Endothelial cells;
RX MEDLINE=92394977; PubMed=1522121;
RA Lampugnani M.G., Resnati M., Raiteri M., Pigott R., Pisacane A.,
RA Hohen G., Ruco L.P., Dejana F.;
RT "A novel endothelial-specific membrane protein is a marker of
cell-cell contacts.";
RT J. Cell Biol. 118:1511-1522(1992).

```

CC CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC CC They preferentially interact with themselves in a homophilic
CC CC manner in connecting cells; cadherins may thus contribute to the
CC CC sorting of heterogeneous cell types. This cadherin may play a
CC CC important role in endothelial cell biology through control of the
CC CC cohesion and organization of the intercellular junctions. It
CC CC associates with alpha-catenin forming a link to the cytoskeleton.
CC CC SUBCELLULAR LOCATION: Type I membrane protein. Found at cell-cell
CC CC boundaries and probably at cell-matrix boundaries.
CC CC -1- TISSUE SPECIFICITY: Endothelial tissues and brain.
CC CC -1- SIMILARITY: Contains 5 cadherin domains.
CC CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD144 entry;
CC CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd144.htm".
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: X79981; CAA56306.1; -
CC CC EMBL: U84722; AAB41796.1; -
CC CC EMBL: AB035304; BAA87418.1; -
CC CC EMBL: X59796; CAA42468.1; -
CC CC PIR: S49893; ICHUC5.
CC CC HSP: P15116; INCU.
CC CC GlycoSiteDB: P3151; -.
CC CC Genew: HGNC:1764; CDH5.
CC CC MIM: 601120; -.
CC CC GO: GO:0005624; C:membrane fraction; TAS.
CC CC GO: GO:0005886; C:plasma membrane; TAS.
CC CC GO: GO:0007156; P:homophilic cell adhesion; TAS.
CC CC InterPro: IPR002126; Cadherin.
CC CC InterPro: IPR000233; Cadherin_C_term.
CC CC Pfam: PF00028; cadherin; 5.
CC CC Pfam: PF01049; Cadherin_C_term; 1.
CC CC PRINTS: PR0205; CADHERIN.
CC CC SMART: SM00112; CA; 5.
CC CC PROSITE: PS00232; CADHERIN_1; 3.
CC CC PROSITE: PS0268; CADHERIN_2; 5.
CC CC KEGG: Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
CC CC KW Signal.
CC CC FT SIGNAL 1 25 POTENTIAL.
CC CC FT PROPEP 26 47 POTENTIAL.
CC CC FT CHAIN 48 784 VASCULAR ENDOTHELIAL-CADHERIN.
CC CC FT DOMAIN 48 593 EXTRACELLULAR (POTENTIAL).
CC CC FT TRANSMEM 594 620 POTENTIAL.
CC CC FT DOMAIN 621 784 CYTOPLASMIC (POTENTIAL).
CC CC FT DOMAIN 48 151 CADHERIN 1.
CC CC FT DOMAIN 152 258 CADHERIN 2.
CC CC FT DOMAIN 259 372 CADHERIN 3.
CC CC FT DOMAIN 373 477 CADHERIN 4.
CC CC FT DOMAIN 478 593 CADHERIN 5.
CC CC FT DOMAIN 736 753 SER-RICH.
CC CC FT CARBOHYD 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 517 517 T -> I (TN REF. 2 AND 4).
CC CC FT CONFLICT 517 517
CC CC FT SEQUENCE 784 AA; 87516 MW; F643BFC22A599DE CRC64;
CC CC -----
CC CC Query Match 100.0%; Score 92; DB 1; Length 784;
CC CC Best Local Similarity 100.0%; Pred. No. 5e-07;
CC CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC CC 1 DWIMQMHIKDKNT 15
CC CC 48 DWIMQMHIKDKNT 62

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CC CC RESULT 2
CC CC CAD5_PIG STANDARD; PRT; 782 AA.
CC CC ID CAD5_PIG
CC CC AC 002840;
CC CC DT 15-JUL-1998 (Rel. 36, Created)
CC CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC CC DT 15-OCT-2001 (Rel. 40, Last annotation update)
CC CC DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5).
CC CC GN CDH5.
CC CC OS Sus scrofa (Pig).
CC CC OX Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC CC OX Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
CC CC OX NCBI_TaxID=9823;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RA Kishaw P.J.;
CC CC RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC CC CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC CC They preferentially interact with themselves in a homophilic
CC CC manner in connecting cells; cadherins may thus contribute to the
CC CC sorting of heterogeneous cell types. This cadherin may play a
CC CC important role in endothelial cell biology through control of the
CC CC cohesion and organization of the intercellular junctions. It
CC CC associates with alpha-catenin forming a link to the cytoskeleton
CC CC (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Found at cell-cell
CC CC boundaries and probably at cell-matrix boundaries (By similarity).
CC CC -1- SIMILARITY: Contains 5 cadherin domains.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: Y13919; CAA74225.1; -
CC CC HSP: P09803; IBDH.
CC CC InterPro: IPR002126; Cadherin.
CC CC InterPro: IPR000233; Cadherin_C_term.
CC CC Pfam: PF00028; cadherin; 5.
CC CC Pfam: PF01049; Cadherin_C_term; 1.
CC CC PRINTS: PR0205; CADHERIN.
CC CC SMART: SM00112; CA; 5.
CC CC PROSITE: PS00232; CADHERIN_1; 3.
CC CC PROSITE: PS0268; CADHERIN_2; 5.
CC CC KEGG: Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
CC CC KW Signal.
CC CC FT SIGNAL 1 22 POTENTIAL.
CC CC FT PROPEP 23 44 POTENTIAL.
CC CC FT CHAIN 45 782 VASCULAR ENDOTHELIAL-CADHERIN.
CC CC FT DOMAIN 45 592 EXTRACELLULAR (POTENTIAL).
CC CC FT TRANSMEM 593 619 POTENTIAL.
CC CC FT DOMAIN 620 782 CYTOPLASMIC (POTENTIAL).
CC CC FT DOMAIN 45 148 CADHERIN 1.
CC CC FT DOMAIN 149 255 CADHERIN 2.
CC CC FT DOMAIN 256 370 CADHERIN 3.
CC CC FT DOMAIN 371 475 CADHERIN 4.
CC CC FT DOMAIN 476 592 CADHERIN 5.
CC CC FT DOMAIN 736 751 SER-RICH.
CC CC FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT SEQUENCE 782 AA; 87546 MW; 7403F974E2DF82F CRC64;
CC CC -----
CC CC Query Match 94.6%; Score 87; DB 1; Length 782;
CC CC Best Local Similarity 100.0%; Pred. No. 3.2e-06;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDBERK 14
 Db 45 DWIMQMHIDBERK 58

RESULT 3
 CAD5_MOUSE
 ID CAD5_MOUSE STANDARD; PRT; 784 AA.
 AC P55284; O35542;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5).
 GN CDH5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain capillary;
 RC MEDLINE=96141083; PubMed=8555485;
 RA Breier G., Breviaro F., Cavada L., Berthier R., Schnerch H.,
 RA Gotisch U., Vestweber D., Risau W., Dejana E.,
 RT "Molecular cloning and expression of murine vascular endothelial-
 RT cadherin in early stage development of cardiovascular system.";
 RL Blood 87:630-641(1996).
 RN [2]
 RP REVISIONS TO 67-70.
 RA Breviaro F.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC STRAIN=BALB/c; TISSUE=Breast carcinoma;
 RX MEDLINE=97364256; PubMed=9220534;
 RA Matsuyoshi N., Toda K.-I., Horiguchi Y., Tanaka T., Nakagawa S.,
 RA Takeuchi M., Imamura S.,
 RT "In vivo evidence of the critical role of cadherin-5 in murine
 RT vascular integrity.";
 RL Proc. Assoc. Am. Physicians 109:362-371(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. This cadherin may play a
 CC important role in endothelial cell biology through control of the
 CC cohesion and organization of the intercellular junctions.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X83930; CAA58782.2; -;
 DR EMBL: D63942; BAA22617.1; -;
 DR EMBL: BC054790; AAH54790.1; -;
 DR HSSP: P15116; INCU.
 DR MGD: MG1:105057; Cdh5.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; cadherin; 5.
 DR Pfam: PF01049; Cadherin_C_term; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 45
 FT CHAIN 46 784
 FT DOMAIN 46 593
 FT TRANSMEM 594 620
 FT DOMAIN 621 784
 FT DOMAIN 46 149
 FT DOMAIN 150 256
 FT DOMAIN 257 371
 FT DOMAIN 372 476
 FT DOMAIN 477 593
 FT DOMAIN 788 753
 FT CARBOHYD 59 59
 FT CARBOHYD 155 155
 FT CARBOHYD 441 441
 FT CARBOHYD 523 523
 FT CARBOHYD 535 535
 SQ SEQUENCE 784 AA, 87902 MW, 7875698DE2F7E160 CRC64;
 Query Match 94.6%; Score 87; DB 1; Length 784;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDBERK 14
 Db 46 DWIMQMHIDBERK 59

RESULT 4
 CADJ_HUMAN
 ID CADJ_HUMAN STANDARD; PRT; 772 AA.
 AC Q9H159;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cadherin-19 precursor (UNC478/PRO941).
 GN CDH19
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20453188; PubMed=10995570;
 RA Koels P., Van Imschoot G., van Roy F.,
 RT "Characterization of three novel human cadherin genes (CDH7, CDH19,
 RT and CDH20) clustered on chromosome 18q22-q23 and with high homology
 RT to chicken cadherin-7.";

```

RL Genomics 68:283-295(2000).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in many tissues, with the exception
CC of uterus.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ007607; CAC13126.1; -
DR EMBL; AY358654; AAC09017.1; -
DR HSSP; P15116; INCU.
DR Genew; HGNC:1758; CDH19.
DR MIM; 603016; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; cadherin_5.
DR PRINTS; PR00205; Cadherin_C_term; 1.
DR SMART; SMO0112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal.
KW SIGNAL.
FT PROPEP 22 43 POTENTIAL.
FT CHAIN 44 772 CADHERIN-19.
FT DOMAIN 44 596 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 597 617 POTENTIAL.
FT DOMAIN 618 772 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 148 CADHERIN_1.
FT DOMAIN 149 256 CADHERIN_2.
FT DOMAIN 257 370 CADHERIN_3.
FT DOMAIN 371 470 CADHERIN_4.
FT DOMAIN 470 581 CADHERIN_5.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 772 AA; 87002 MW; 650AD27480343C39 CRC64;
Query Match 62.0%; Score 57; DB 1; Length 772;
Best Local Similarity 57.1%; Pred. No. 0.19;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 WIMQNHIDEKNT 15
DB 45 WYMNQFVEEMNT 58

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GN CDH8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10861224;
RA Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
RT "Identification of three human type-II classic cadherins and frequent
RT heterophilic interactions between different subclasses of type-II
RT classic cadherins.";
RL Biochem. J. 349:159-167(2000).
RN [2]
RP SEQUENCE OF 7-799 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95073006; PubMed=7982033;
RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin.";
RL Cell Adhes. Commun. 2:15-26(1994).
RN [3]
RP SEQUENCE OF 294-799 FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins
RT in nervous tissue.";
RL Cell Regul. 2:261-270(1991).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
CC nerve cell lines, such as retinoblasts, glioma cells and
CC neuroblasts.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC -----
DR EMBL; AB035305; BAA87419.1; -
DR EMBL; U34060; AAA35628.1; ALT_INIT.
DR HSSP; P15116; INCU.
DR Genew; HGNC:1767; CDH8.
DR MIM; 603008; -
DR GO; GO:0007155; P:cell adhesion; TAS.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR00233; Cadherin_C_term.
DR Pfam; PF00028; cadherin_5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SMO0112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal.
KW SIGNAL.
FT PROPEP 1 29 POTENTIAL.
FT CHAIN 30 61 CADHERIN-8.
FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 622 642 POTENTIAL.
FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 62 167 CADHERIN_1.
FT DOMAIN 168 276 CADHERIN_2.
FT DOMAIN 277 391 CADHERIN_3.

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FT DOMAIN 392 494 CADERIN 4.
FT DOMAIN 495 616 CADERIN 5.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 355 355 V -> D (IN REF. 2 AND 3).
FT CONFLICT 647 647 H -> HQ (IN REF. 2 AND 3).
SQ SEQUENCE 799 AA; 88253 MW; 9B119B86039C6A0A CRC64;

Query Match 53.3%; Score 49; DB 1; Length 799;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WIMNOMHIDE 12
DB 63 WWMNOMFVLEE 73

RESULT 6
CAD8 MOUSE STANDARD; PRT; 799 AA.
ID CAD8_MOUSE
AC P97291;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cadherin-8 precursor.
GN CDH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=97174321; PubMed=9022055;
RA Korematsu K., Redies C.;
RT "Restricted expression of cadherin-8 in segmental and functional
subdivisions of the embryonic mouse brain.";
RL Dev. Dyn. 208:178-189(1997).
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells; cadherins may thus contribute to the
sorting of heterogeneous cell types.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 5 cadherin domains.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X95600; CAA64857.1; -
DR HSSP; P15116; INCU.
DR MGd; WGI:107434; Cdh8.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF00028; cadherin_5.
DR Pfam; PF01049; Cadherin_C-term; 1.
DR PRINTS; PR00205; CADERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00332; CADERIN 1; 3.
DR PROSITE; PS00268; CADERIN 2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 61 POTENTIAL.
FT CHAIN 62 799 CADERIN-8.

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FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 622 642 POTENTIAL.
FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 62 167 CADERIN 1.
FT DOMAIN 168 276 CADERIN 2.
FT DOMAIN 277 391 CADERIN 3.
FT DOMAIN 392 494 CADERIN 4.
FT DOMAIN 495 616 CADERIN 5.
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

Query Match 53.3%; Score 49; DB 1; Length 799;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WIMNOMHIDE 12
DB 63 WWMNOMFVLEE 73

RESULT 7
CAD8 RAT STANDARD; PRT; 799 AA.
ID CAD8_RAT
AC O54800; O54801;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-8 precursor.
GN CDH8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=98190518; PubMed=9521872;
RA Kido M., Obara S., Tanihara H., Koehelle J.M., Seldin M.F.,
RA Taketani S., Suzuki S.T.;
RT "Molecular properties and chromosomal location of cadherin-8.";
RL Genomics 48:186-194(1998).
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells; cadherins may thus contribute to the
sorting of heterogeneous cell types.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=O54800-1; Sequence=Displayed;
Name=2;
IsoId=O54800-2; Sequence=VSP 000638, VSP 000639;
CC -!- SIMILARITY: Contains 5 cadherin domains.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB010436; BAA24452.1; -
DR EMBL; AB010437; BAA24453.1; -
DR HSSP; P15116; INCU.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF00028; cadherin_5.
DR Pfam; PF01049; Cadherin_C-term; 1.
DR PRINTS; PR00205; CADERIN.

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DR					SMART; SMO0112; CA; 5.
DR					PROSITE; PS00232; CADERIN_1; 3.
KW					PROSITE; PSS0268; CADERIN_2; 5.
KW					Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW					Signal; Alternative splicing.
FT	SIGNAL	1	29	POTENTIAL.	
FT	PROPEP	30	61	POTENTIAL.	
FT	CHAIN	62	799	CADERIN-8.	
FT	DOMAIN	62	621	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	622	642	POTENTIAL.	
FT	DOMAIN	643	799	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	62	167	CADERIN 1.	
FT	DOMAIN	168	276	CADERIN 2.	
FT	DOMAIN	168	391	CADERIN 3.	
FT	DOMAIN	392	494	CADERIN 4.	
FT	DOMAIN	495	616	CADERIN 5.	
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	473	473	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	544	544	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	VARSPLIC	514	532	IQTYSANDKDDPKNGHFFL -> NISMLLNKVFVNCFLV N (in isoform 2) . /Fric=VSP 000638. Missing (in isoform 2) .	
FT	VARSPLIC	533	799	Missing (in isoform 2) . /Fric=VSP 000639.	
QO	SEQUENCE	799 AA;	88332 MW;	FOLDID45A80966CB6 CXC64;	

Query Match	53.3%;	Score 49;	DB 1;	Length 799;
Best Local Similarity	63.6%;	Pred. No. 3.8;		
Matches	7;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;

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QY      2 W I W N Q M H I D E E 1 2
        | : | | | | : | |
Db      6 3 W V W N Q M F V L E E 7 3
```

RESULT 8

CHICKEN	STANDARD;	PRT;	792 AA.
ID_CADB_CHICK			

DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Cadherin-11 precursor.

05 Gallus gallus (Chicken).
06
07 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
08 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae

OK NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.
CC STRAIN-White Tobacco;

RA Wei J., Dong X.R., Topouzis S.
RA Kotelianskij V., Majesky M.W.:

RT smooth muscle differentiation

-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins

sorting of heterogeneous cell types.

CC -!- SIMILARITY: Contains 5 cadherin domains

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CC - Bureau of Small Business Administration

	EMBL; AF055342; AAC3675.1; -	
DR	InterPro; IPR002126; Cadherin.	
DR	InterPro; IPR00233; Cadherin_C_term.	
DR	Pfam; PF00028; cadherin; 5.	
DR	Pfam; PR01049; Cadherin_C term; 1.	
DR	PRINTS; PR00205; CADHERIN_	
DR	SMART; SM00112; CA; 5.	
DR	PROSITE; PS00232; CADHERIN_1; 3.	
DR	PROSITE; PS0268; CADHERIN_2; 5.	
KW	Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;	
	Signal.	
FT	SIGNAL	1..22
FT	PROPEP	23..53
FT	CRAIN	54..792
FT	DOMAIN	54..613
FT	TRANSMEM	614..634
FT	DOMAIN	635..792
FT	DOMAIN	54..159
FT	DOMAIN	160..268
FT	DOMAIN	269..383
FT	DOMAIN	384..486
FT	DOMAIN	487..608
FT	CARBOHYD	455..455
FT	CARBOHYD	536..536
FT	CARBOHYD	594..594
SQ	SEQUENCE	792 AA; 87572 MW; 333498C6686731AB CRC64;

Query Match	48.9%	Score 45	DB 1	Length 124
Best Local Similarity	54.5%	Pred. No. 16		
Matches 6; Conservative		Mismatches 3	Indels 0	Gaps 0

QY	2	W1WNQMHIDEE	12
		1:111	:11
Db	55	W1WNQFFVIEE	65

RESULTS

ID	CADB HUMAN	STANDARD;	PRT;	796 AA
AC	P55287	015065	091093	09U094

DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last amottion update)
DE	Cadherin-11 precursor (Osteoblast-cadherin) (OSF-4)
DE	Cadherin-11 precursor (Osteoblast-cadherin) (OSF-4)

OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI TaxID: 9606.

```

RN      [1]
PD      SENTENCE FROM N.A. (ISOFORM 1) .

```

```

RC      I1SS0E=Brain;
RX      MEDLINE=95073006; PubMed=7982033;

```

RT "Cloning of five human cadherins clarifies characteristic

structurally different types of cadherin." ;

RN [2] SCIENCE FROM N A (TSOFORMS 1 ANT

RX MEDLINE=94216322; PubMed=8163513;
PA Okazaki M, Takeshita S, Kawai S, Kikuno R, Tsujimura A.

RT "Molecular cloning and characterization of OB-

RL J. Biol. Chem. 269:12092-12098 (1994).

SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1)

RX MEDLINE=91283540; PubMed=20596658;

RT "Diversity of the cadherin family: evidence for eight new cadherins

RT in nervous tissue";
 RL Cell Regul. 2:261-270(1991).
 RN [4]
 RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 RA Kools P.E.J., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.;
 RT "Alternative cadherin-11 transcripts encoding truncated adhesion
 RL molecules are detectable in both human cancer and normal cells";
 CC Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P55287-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P55287-2; Sequence=VSP_000640; VSP_000641;
 CC
 CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 CC other tissues. Expressed in neuroblasts.
 CC
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC -----
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 CC -----
 CC EMBL; I34056; AAA5622.1; -
 CC EMBL; D21254; BAA04798.1; -
 CC EMBL; D21255; BAA04799.1; -
 CC EMBL; AF060370; AAD27755.1; -
 CC EMBL; AF060369; AAD27755.1; JOINED.
 CC EMBL; AF060370; AAD27756.1; -
 CC EMBL; AF060369; AAD27756.1; -
 CC PIR: A38992; A38992.
 CC HSSP: P5116; INCT.
 CC
 CC GeneW; HGNC:1750; CDH11.
 CC MIM; 600023; -
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0007156; P:homophilic cell adhesion; NAS.
 CC GO; GO:0001503; P:specificity; NAS.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C-term.
 CC Pfam; PF00028; cadherin_5.
 CC Pfam; PF01049; Cadherin_C-term; 1.
 CC PRINTS; PR00205; CADHERIN.
 CC SMART; SM00112; CA: 5
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 CC Signal; Alternative splicing.
 CC
 CC SIGNAL 1 22
 CC PROPEP 23 53
 CC CHAIN 54 796
 CC DOMAIN 54 796
 CC TRANSMEM 618 640
 CC TRANSMEM 618 640
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC CADHERIN 1.
 CC CADHERIN 2.
 CC CADHERIN 3.
 CC CADHERIN 4.
 CC CADHERIN 5.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC VIVVPTLRQKREPLVFEEDRENTITDYDGGGEED
 CC TEADRIATLQPDGNGFTIP -> GCSLTPSPSPRDMR
 CC LLYLGQLMFSYKVNRFGLGVFIKPLPLVVAATSPST
 CC TLTSL (in isoform 2).
 CC /FTid=VSP_000640.

FT VARSPLIC 694 796 Missing (in isoform 2).
 FT FT CONFLICT 271 272 /FTid=VSP_000641.
 FT FT CONFLICT 275 275 RL -> SV (IN REF. 2).
 FT FT CONFLICT 340 340 M -> I (IN REF. 2).
 FT FT CONFLICT 343 343 E -> K (IN REF. 2).
 FT FT CONFLICT 373 373 S -> A (IN REF. 2).
 FT FT CONFLICT 471 471 Q -> K (IN REF. 2).
 SO SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB2E CRC64;
 Query Match 48.9%; Score 45; DB 1; Length 796;
 Best Local Similarity 54.5%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 WINNQMHHDE 12
 Db 55 WYNNQFFVIEH 65
 RESULT 10
 CADB_MOUSE STANDARD; PRT; 796 AA.
 AC P55288;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 15-MAR-2004 (rel. 43, Last annotation update)
 DE Cadherin-11 precursor (osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN CDH11 OR CAD-11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269886; PubMed=7750649;
 RA Hoffmann I.H., Balling R.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RT cadherin";
 RL Dev. Biol. 169:337-346(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RT in the head, somite, and limb bud of early mouse embryos";
 RL Dev. Biol. 169:347-358(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amann E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullen P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bullyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvedchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA	Rodriguez A.C., Grimwood J., Schmutz Z.J., Myers R.M.,
RA	Battifield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schmeck A., Schein J.E., Jones S.J.W., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[5]
RP	DEVELOPMENTAL STAGE.
RC	STRAIN=C57BL/6; TISSUE=Testis;
PX	MEDLINE=97033837; PubMed=8879495;
RA	Munro S.B., Blaschuk O.W.,
RT	"A comprehensive survey of the cadherins expressed in the testes of
RT	fetal, immature, and adult mice utilizing the polymerase chain
RT	reaction.";
RL	Biol. Reprod. 55:822-827(1996).
CC	-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC	They preferentially interact with themselves in a homophilic
CC	manner in connecting cells; cadherins may thus contribute to the
CC	sorting of heterogeneous cell types.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
CC	lines, precursor cell lines of osteoblasts, and primary
CC	osteoblastic cells from calvaria, as well as in lung, testis, and
CC	brain tissues at low levels.
CC	-1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
CC	gonad and decreases 8-fold in newborn.
CC	-1- SIMILARITY: Contains 5 cadherin domains.
CC	-----
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CC	or send an email to license@isb-sib.ch). -----
DR	EMBL; X77557; CAA54674.1; -.
DR	EMBL; D31963; BA06730.1; -.
DR	EMBL; D21253; BA04797.1; -.
DR	EMBL; BC046314; AAH46314.1; -.
DR	PIR; A53584; A53584.
DR	PIR; I48277; I48277.
DR	PIR; I49556; I49556.
DR	HSSP; P15116; INCT.
DR	MGD; MG1:99217; cdhl1.
DR	GO; GO:0005737; C:cytosolasm; IDA.
DR	GO; GO:0005886; C:plasma membrane; IDA.
DR	InterPro; IPRO02126; Cadherin.
DR	InterPro; IPRO00223; Cadherin_c_term.
DR	pfam; PF00028; cadherin_5.
DR	PRFam; PRF01049; Cadherin_C_term; 1.
DR	PRINTS; PRO0205; CADHERIN.
DR	SMART; SM00112; CA; 5.
DR	PROSITE; PS00232; CADHERIN_1; 3.
DR	PROSITE; PS00268; CADHERIN_2; 5.
KW	Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KM	Signal.
FT	SIGNAL. 1 24 POTENTIAL.
FT	PROPEP 25 53 POTENTIAL.
FT	CHAIN 34 796 CADHERIN_11.
FT	DOMAIN 54 617 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 618 640 POTENTIAL.
FT	DOMAIN 641 796 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 54 159 CADHERIN 1.
FT	DOMAIN 160 268 CADHERIN 2.
FT	DOMAIN 269 383 CADHERIN 3.
FT	DOMAIN 384 486 CADHERIN 4.
FT	DOMAIN 487 612 CADHERIN 5.
FT	CARDHYD 455 455 N-LINKED (GLCNAC..) (POTENTIAL).
FT	CARDHYD 540 540 N-LINKED (GLCNAC..) (POTENTIAL).
FT	CONFLICT 462 462 E -> D (IN REF. 1).
FT	CONFLICT 589 589 T -> L (IN REF. 2).
FT	CONFLICT 655 655 D -> N (IN REF. 2).

```

FT CONFLICT 751 751 V -> M (IN REF. 1) .
FT CONFLICT 777 777 P -> Q (IN REF. 2) .
FT CONFLICT 782 782 L -> P (IN REF. 2) .
SQ SEQUENCE 796 AA, 88112 MW, 0D56AD24641DD529 CRC64;

Query Match 48.9%; Score 45; DB 1; Length 796;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Ox 2 WINNOMHIDE 12
Db 55 WWMQFPVIE 65

RESULT 11
CADM_MOUSE
ID CADM_MOUSE STANDARD; PRT; 813 AA.
AC QWRT5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-22 precursor (PB-cadherin) .
OS CDH22.
OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Cranicia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=99326347; PubMed=10398531;
RA Kitaajima K., Koshimizu U., Nakamura T.;
RA "Expression of a novel type of classic cadherin, PB-cadherin in
RT developing brain and limb buds.";
RL Dev. Dyn. 215:206-214(1999) .
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. PB-cadherin may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain. Abundant in
CC olfactory bulb, cerebrum, and cerebellum, less in pons, medulla,
CC and spinal cord. Low expression in heart. No expression in lung,
CC liver, spleen, kidney, testis, stomach, intestine, colon, and
CC placenta.
CC -1- DEVELOPMENTAL STAGE: Expressed at 9.5 dpc onwards. At 10.5 dpc, in
CC brain (telencephalic vesicles and isthmus), spinal cord and limb
CC buds (in the zone of polarizing activity). At 14.5 dpc, in
CC olfactory bulb and cerebellum.
CC -1- INDUCTION: Down-regulated by thyroid hormone.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC
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CC or send an email to license@sib-sib.ch) .
CC
CC -----
CC EMBL, AB019618, BAA34426.1, -
CC MGD, MG1:1341843, Cdh22.
CC HSSP, PG5116, INCI.
CC InterPro, IPR002326, Cadherin.
CC InterPro, IPR000253, Cadherin_C_term.
CC Pfam, PF00028, cadherin_5.
CC Pfam, PF01049, Cadherin_C_term_1.
CC PRINTS, PRO0205, CADHERIN.
CC SMART, SM00112, CA: 5.
CC PROSITE, PS00232, CADHERIN_1; 2.
CC PROSITE, PS0268, CADHERIN_2; 5.

```

KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 33 POTENTIAL.
 FT CHAIN 34 813 CADHERIN-22.
 FT DOMAIN 33 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 813 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 61 165 CADHERIN 1.
 FT DOMAIN 166 274 CADHERIN 2.
 FT DOMAIN 275 391 CADHERIN 3.
 FT DOMAIN 392 495 CADHERIN 4.
 FT DOMAIN 496 613 CADHERIN 5.
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 813 AA; 88021 MW; 5510F9848D976567 CRC64;
 Query Match 48.9%; Score 45; DB 1; Length 813;
 Best Local Similarity 54.5%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 WIMQMHIDEE 12
 Db 61 WWMNQFFVVEE 71
 RESULT 12
 CADM_RAT STANDARD; PRT; 813 AA.
 AC Q63315; Q63561; 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cadherin-22 precursor (PB-cadherin).
 OS CDH22.
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
 RC STRAIN=WiStar; TISSUE=Brain, and Pituitary;
 MEDLINE=96212232; PubMed=8626716;
 RA Sugimoto K., Honda S., Yamamoto T., Ueki T., Monden M., Kaji A.,
 RA Matsunoto K., Nakamura T.,
 RT "Molecular cloning and characterization of a newly identified member
 of the cadherin family, PB-cadherin.";
 RL J. Biol. Chem. 271:11548-11556(1996).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 They preferentially interact with themselves in a homophilic
 manner in connecting cells; cadherins may thus contribute to the
 sorting of heterogeneous cell types. PB-cadherins may have a role
 in the morphological organization of pituitary gland and brain
 tissues.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=1;
 IsoId=Q63315-1; Sequence=Displayed;
 Name=2;
 IsoId=Q63315-2; Sequence=VSP_000643, VSP_000644;
 Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Strongly expressed in the pituitary gland and
 the brain (in the inner granular and glomerular layers of the
 olfactory bulb, anterior olfactory nucleus, primary olfactory
 cortex, Purkinje cell layer of cerebellum, and pineal gland). Low
 expression in lung and heart. No expression in submandibular
 gland, thymus, liver, spleen, adrenal, and kidney.
 CC -!- DEVELOPMENTAL STAGE: Expressed strongly in fetal brain.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D83348; BAA11894.1; -;
 DR EMBL; D83349; BAA11895.1; -;
 DR HSSP; P15116; INCU.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; cadherin; 5.
 DR Pfam; PF01049; cadherin_C-term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 33 POTENTIAL.
 FT CHAIN 34 813 CADHERIN-22.
 FT DOMAIN 33 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 813 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 61 165 CADHERIN 1.
 FT DOMAIN 166 274 CADHERIN 2.
 FT DOMAIN 275 391 CADHERIN 3.
 FT DOMAIN 392 495 CADHERIN 4.
 FT DOMAIN 496 613 CADHERIN 5.
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 668 694 NDEGGGEOTFAYDMSALRSYDFGL -> ITGSGHRGTS
 NDEHQCRPSISLGRKP (in isoform 2).
 FT VARSPLIC 695 813 /FTId=VSP_000643.
 FT VARSPLIC 813 Missing (in isoform 2).
 FT VARSPLIC /FTId=VSP_000644.
 SQ SEQUENCE 813 AA; 87978 MW; 30BEA60B5D2D467B CRC64;
 Query Match 48.9%; Score 45; DB 1; Length 813;
 Best Local Similarity 54.5%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 WIMQMHIDEE 12
 Db 61 WWMNQFFVVEE 71
 RESULT 13
 CADM_HUMAN STANDARD; PRT; 819 AA.
 ID CADM_HUMAN
 AC Q86UF0; Q86UP1; Q9N784;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cadherin-24 precursor (UMQ2834/PRO34009).
 GN CDH24 OR CDH11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
 RP CATEININS.
 RX MEDLINE=22753805; PubMed=12734196;
 RA Karafiasz B.J., Nieman M.T., Wheelock M.J., Johnson K.R.,
 RT "Characterization of cadherin-24, a novel alternatively spliced type
 II cadherin.";
 RL J. Biol. Chem. 278:27513-27519 (2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,


```

CC tissues (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL031687; CAB51587.2; -.
CC EMBL; AF035300; AAB88183.1; -.
CC Genew; HGNC:13251; CDH22.
CC HSSP; P15116; 1NCJ.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR000233; Cadherin_C_term.
CC Pfam; PF00028; cadherin; 5.
CC PRINTS; PR00205; Cadherin_C_term; 1.
CC SMART; SM00112; CA; 5.
CC PROSITE; PS00232; CADHERIN_1; 2.
CC PROSITE; PS00268; CADHERIN_2; 5.
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
CC Signal.
CC KW SIGNAL.
CC FT CHAIN 1 34 POTENTIAL.
CC FT PROPEP 35 828 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 625 624 POTENTIAL.
CC FT DOMAIN 646 828 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 169 168 CADHERIN_1.
CC FT DOMAIN 278 394 CADHERIN_2.
CC FT DOMAIN 395 498 CADHERIN_3.
CC FT DOMAIN 439 616 CADHERIN_4.
CC FT DOMAIN 466 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 466 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 826 AA; 89091 MW; 520781D1F624DCA CRC64;

Query Match 48.9%; Score 45; DB 1; Length 828;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WIMNQMHIIDE 12
Db 64 WVMNQFVLEE 74

RESULT 15
CAD7 CHICK STANDARD; PRT; 785 AA.
AC Q90763.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cadherin-7 precursor.
GN CDH7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Brain;
RX MEDLINE=95309115; PubMed=7540531;
RA Nakagawa S., Takeichi M.;
RT "Neural crest cell-cell adhesion controlled by sequential and
RT subpopulation-specific expression of novel cadherins.";
RL Development 121:1321-1332(1995).
-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.

```

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CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D42150; BAA07721.1; -.
CC PIR; I50180; I50180.
CC HSSP; P15116; 1NCH.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR000233; Cadherin_C_term.
CC Pfam; PF00028; cadherin; 5.
CC PRINTS; PR00205; Cadherin_C_term; 1.
CC SMART; SM00112; CA; 5.
CC PROSITE; PS00232; CADHERIN_1; 3.
CC PROSITE; PS00268; CADHERIN_2; 5.
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
CC Signal.
CC KW SIGNAL.
CC FT CHAIN 1 27 POTENTIAL.
CC FT PROPEP 28 47 POTENTIAL.
CC FT TRANSMEM 48 785 CADHERIN-7.
CC FT DOMAIN 48 607 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 608 628 POTENTIAL.
CC FT DOMAIN 629 785 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 49 153 CADHERIN_1.
CC FT DOMAIN 262 377 CADHERIN_2.
CC FT DOMAIN 263 377 CADHERIN_3.
CC FT DOMAIN 378 482 CADHERIN_4.
CC FT DOMAIN 482 599 CADHERIN_5.
CC FT CARBOHYD 449 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 785 AA; 87171 MW; 895B06D8141B34D4 CRC64;

Query Match 47.8%; Score 44; DB 1; Length 785;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WIMNQMHIIDE 12
Db 49 WVMNQFVLEE 59

```

Search completed: July 29, 2004, 11:35:23
Job time : 7.66667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 11:31:25 ; Search time 10.333 Seconds
(without alignments)
139.633 Million cell updates/sec

Title: US-10-040-128-3
Perfect score: 92
Sequence: 1 DWIMQMIDEKNT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	784	1 IJHUC5	cadherin 5 precursor - human
2	49	53.3	793	2 D38992	cadherin 8 - human
3	48	52.2	524	2 T20872	hypothetical prote
4	45	48.9	796	2 A38992	cadherin 11 precursor
5	45	48.9	796	2 I48277	cadherin-11 - mous
6	45	48.9	796	2 I49556	cadherin-11 - mous
7	45	48.9	796	2 A53584	OB-cadherin precursor
8	44.5	48.4	963	2 T09911	probable serine/th
9	44	47.8	500	2 B89962	hypothetical prote
10	44	47.8	785	2 I50180	cadherin-7 - chick
11	44	47.8	790	2 I51638	F-cadherin - Afric
12	44	47.8	790	2 G02678	cadherin-14 - huma
13	44	47.8	794	2 I59372	cadherin 12 - huma
14	43	46.7	435	2 C84941	histidinol dehydro
15	42.5	46.2	388	1 D70006	conserved hypothet
16	42	45.7	82	2 T46510	hypothetical prote
17	42	45.7	296	2 F95380	probable hydrolase
18	42	45.7	315	2 A35335	dipeptide transpor
19	42	45.7	427	2 AF0590	citrate synthase l
20	42	45.7	529	2 T21575	hypothetical prote
21	42	45.7	907	2 B66692	probable wall-asso
22	41.5	45.1	392	2 S54888	probable NADPH deh
23	41.5	45.1	1032	2 T43257	beta-1,3 exoglucan
24	41	44.6	77	2 A11306	hypothetical prote
25	41	44.6	314	2 S47696	nucleic transport s
26	41	44.6	314	2 H91171	transport of nicle
27	41	44.6	314	2 H86017	transcript of nicle
28	41	44.6	431	2 B82119	citrate synthase V
29	41	44.6	519	2 T33616	hypothetical prote

30	41	44.6	532	2 G90607	hypothetical prote
31	41	44.6	619	2 B97668	hypothetical prote
32	41	44.6	619	2 AG2892	hypothetical prote
33	41	44.6	712	2 T16338	hypothetical prote
34	41	44.6	770	2 S11161	hypothetical prote
35	41	44.6	789	2 I52701	anthranilate synth
36	41	44.6	790	2 I37016	K-cadherin - rat
37	41	44.6	790	2 I50178	cadherin-6 - human
38	41	44.6	2241	2 T20971	hypothetical prote
39	41	44.6	2261	2 T20978	hypothetical prote
40	41	44.6	6831	2 A88852	protein unc-22 (im
41	41	44.6	6839	2 S57242	twistacin [similari
42	41	44.6	7160	2 T27935	hypothetical prote
43	40	43.5	77	2 A11678	hypothetical prote
44	40	43.5	120	2 C72425	hypothetical prote
45	40	43.5	200	1 G64106	3-isopropylmalate

ALIGNMENTS

RESULT 1
IJHUC5
cadherin 5 precursor - human
N/Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text change 22-Jun-1999
C/Accession: S49893; S24305; A43418
R/Breviario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov
A/Reference number: S49893
A/Accession: S49893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-784 <BEB>
A/Cross-references: EMBL:X79981; NID:G599833; PIDN:CAA56306.1; PID:G599834
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: S24305
A/Molecule type: mRNA
A/Residues: 5-516, 'I', 518-784 <SUZ>
A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CAA42468.1; PID:G29593
R/Lampugnani, M.G.; Resnati, M.; Rattieri, M.; Pigotti, R.; Pissacane, A.; Houen, G.; Ruco,
J. Cell Biol. 118, 1511-1522, 1992
A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
A/Reference number: A43418; MUID:92394977; PMID:1522121
A/Accession: A43418
A/Molecule type: protein
A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-
A/Experimental source: cultured endothelial cells
A/Note: sequence extracted from NCBI Backbone (NCBIP:113040, NCBIP:113045, NCBIP:113047,
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
C/Genetics:
A/Genes: GDB:CDH5
A/Cross-references: GDB:134230; OMIM:601120
A/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-47/Domain: propeptide #status predicted <PRO>
F/48-784/Product: cadherin 5 #status predicted <MAT>
F/48-593/Domain: extracellular #status predicted <EXT>
F/50-151/Domain: cadherin repeat homology <CR1>
F/154-258/Domain: cadherin repeat homology <CR2>
F/261-372/Domain: cadherin repeat homology <CR3>
F/375-479/Domain: cadherin repeat homology <CR4>
F/481-587/Domain: cadherin repeat homology <CR5>
F/594-620/Domain: transmembrane #status predicted <TM>
F/621-784/Domain: intracellular #status predicted <INT>
F/736-753/Region: serine-rich

F:61,112,157,362,442,523,535/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 92; DB 1; Length 784;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWIMQMHIDEKNT 15
|||:|||||
Db 48 DWIMQMHIDEKNT 62

RESULT 2

D38992
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous ti
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:J34060; NID:g506411; PID:AA35628.1; PID:g506412
C:Genetics:
A:Gene: GDB:CDH8
A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 53.3%; Score 49; DB 2; Length 793;
Best Local Similarity 63.6%; Pred. No. 6.2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 WIMQMHIDE 12
|||:||||
Db 56 WIMQMFVLEE 66

RESULT 3

T20872
hypothetical protein F26H9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T20872; T21443
R: Sims, M.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19337
A:Accession: T20872
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <WIL>
A:Cross-references: EMBL:Z75535; PIDN:CAA99829.1; GSPDB:GN00019; CESP:F26H9.1
A:Experimental source: clone F14B4
R: Baynes, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19422

A:Accession: T21443
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <W12>
A:Cross-references: EMBL:Z81516; PIDN:CA804206.1; GSPDB:GN00019; CESP:F26H9.1
A:Experimental source: clone F26H9
C:Genetics:
A:Gene: CESP:F26H9.1
A:Map position: 1
A:Insertions: 49/2; 99/1; 136/1; 186/1; 228/3; 287/3; 346/1; 403/1; 449/3

Query Match 52.2%; Score 48; DB 2; Length 524;
Best Local Similarity 53.8%; Pred. No. 5.7;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 WIMQMHIDEKNT 14
|||:|||||
Db 486 WDMQKRNIDEHRN 498

RESULT 4

A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C:Accession: A38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous ti
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: A38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <SUZ>
A:Cross-references: GB:J34056; NID:g506403; PIDN:AA35622.1; PID:g506404
C:Genetics:
A:Gene: GDB:CDH11; OB
A:Cross-references: GDB:512891; OMIM:600023
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:56-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:271-383/Domain: cadherin repeat homology <CR3>
F:386-488/Domain: cadherin repeat homology <CR4>

Query Match 48.9%; Score 45; DB 2; Length 796;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WIMQMHIDE 12
|||:||||
Db 55 WIMQMFVLEE 65

RESULT 5

I48277
cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I48277
R:Hoffmann, T.; Bailing, R.
Dev. Biol. 169, 337-346, 1995
A:Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A:Reference number: I48277; MUID:95269886; PMID:7750649
A:Accession: I48277
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <RES>
A:Cross-references: EMBL:X77557; NID:g642796; PIDN:CAA54674.1; PID:g666071
C:Genetics:
A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology <CDH>
F:56-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 45; DB 2; Length 796;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WIMQMHIDE 12
|||:||||
Db 55 WIMQMFVLEE 65

RESULT 6

I49556
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C/Accession: I49556
R/Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A/Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A/Reference number: I49556; MUID:9526887; PMID:7750650
A/Accession: I49556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: GB:D31963; NID:9974190; PIDN:BAA06730.1; PID:9974191
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 45; DB 2; Length 796;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNNQMHIDE 12
Db 55 WNNQFVLEE 65

RESULT 7
A53584
OB-cadherin precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
C/Accession: A53584
R/Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Maam, E.
J. Biol. Chem. 269, 12092-12098, 1994
A/Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A/Reference number: A53584; MUID:94216322; PMID:8163513
A/Accession: A53584
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-796 <OKA>
A/Cross-references: GB:D1253; NID:9994774; PIDN:BAA04797.1; PID:9994775
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: transmembrane protein
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 48.9%; Score 45; DB 2; Length 796;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNNQMHIDE 12
Db 55 WNNQFVLEE 65

RESULT 8
T09911
Probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C/Accession: T09911
R/Beyan, M.; Zimmermann, W.; Grensien, A.; Mamut, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, June 1999
A/Reference number: Z16896
A/Accession: T09911
A/Molecule type: DNA
A/Residues: 1-963 <BEV>
A/Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.310
A/Experimental source: cultivar Columbia; BAC clone T22A6
C/Genetics:
A/Gene: ATSP:T22A6.310
A/Map position: 4

A/Introns: 286/3; 386/2; 434/3; 473/2; 543/1; 678/1; 691/3; 719/3; 753/2; 788/3; 821/3;
C/Keywords: phosphotransferase; protein kinase

Query Match 48.4%; Score 44.5; DB 2; Length 963;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 DWI---NWNQMHIDE 11
Db 660 DWLEVSNNELHIKE 673

RESULT 9
E89962
Hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: E89962
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cuí, L.; Ogu
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirata, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: E89962
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-500 <KUR>
A/Cross-references: GB:BA000018; PID:913701565; PIDN:BAB42858.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA1590

Query Match 47.8%; Score 44; DB 2; Length 500;
Best Local Similarity 41.7%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DWI---NWNQMHIDE 12
Db 318 WNNQSLIEDQ 329

RESULT 10
I50180
cadherin-7 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I50180
R/Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: I50178; MUID:95309115; PMID:7540531
A/Accession: I50180
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-785 <NAK>
A/Cross-references: GB:D42150; NID:9868000; PIDN:BAA07721.1; PID:9868001
C/Superfamily: cadherin; cadherin repeat homology
F/156-262/Domain: cadherin repeat homology <CDH>

Query Match 47.8%; Score 44; DB 2; Length 785;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNNQMHIDE 12
Db 49 WNNQFVLEE 59

RESULT 11
I51638
F-cadherin - African clawed frog
C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C/Accession: 151638; S55391
R:Rameseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A/Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A/Reference number: 151638; MUID:96039533; PMID:7496627
A/Accession: 151638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <ESP>
A/Cross-references: EMBL:X85330; NID:9854634; PIDN:CAA59679.1; PID:9854635
C/Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 47.8%; Score 44; DB 2; Length 790;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WINQMHIIDE 12
Db 54 WVMNQFVLEE 64

RESULT 12
G02678
cadherin-14 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 21-Jan-2000
C/Accession: G02678
R:Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A/Accession: G02678
A/Reference number: H01584
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <SHI>
A/Cross-references: EMBL:U59325; NID:G1389852; PIDN:AA802933.1; PID:G1389853
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 47.8%; Score 44; DB 2; Length 790;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WINQMHIIDE 12
Db 55 WVMNQFVLEE 65

RESULT 13
I59372
cadherin 12 - human
N/Alternate names: Br-cadherin
C/Species: Homo sapiens (man)
C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 20-Aug-1999
C/Accession: I59372
R:Sellig, S.; Bruno, S.; Scharf, U.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.M.
Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
A/Title: Expressed cadherin pseudogenes are localized to the critical region of the spri
A/Reference number: I59372; MUID:95249541; PMID:7731968
A/Accession: I59372
A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A/Molecule type: mRNA
A/Residues: 1-794 <RNS>
A/Cross-references: GB:U3477; NID:G793942; PIDN:AA848539.1; PID:G793943
C/Genetics:
A/Gene: GDB:CDH12
A/Cross-references: GDB:596324
A/Map position: SP13-SP14
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:57-160/Domain: cadherin repeat homology <CR1>
F:163-269/Domain: cadherin repeat homology <CR2>

F:272-384/Domain: cadherin repeat homology <CR3>
F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <IN>

Query Match 47.8%; Score 44; DB 2; Length 794;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WINQMHIIDE 12
Db 56 WVMNQFVLEE 66

RESULT 14
C84941
histidinol dehydrogenase (EC 1.1.1.23) [imported] - Buchnera sp. (strain APS)
C/Species: Buchnera sp.
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C/Accession: C84941
R:Shigenobu, S.; Mitanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A/Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A/Reference number: A84930; MUID:20445173; PMID:10993077
A/Accession: C84941
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-435 <STO>
A/Cross-references: GB:AP000398; GSPDB:GN00144
A/Experimental source: strain APS
C/Genetics:
A/Gene: hsd; BU100
C/Superfamily: histidinol dehydrogenase; histidinol dehydrogenase homology
C/Keywords: oxidoreductase

Query Match 46.7%; Score 43; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 WNMQHIDEK 13
Db 10 WNKHPDECK 19

RESULT 15
D70006
conserved hypothetical protein yubA - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C/Accession: D70006
R:Kunert, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berr
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
A/Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
A/Authors: Tamakoshi, A.; Tanaka, T.; Tetsuya, P.; Tognoni, A.; Tostato, V.; Uchiyama
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancho, K.; Yata, K.; Yoshida, J
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: D70006
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-388 <KUN>
A/Cross-references: GB:D99119; GB:AL009126; NID:G2635411; PIDN:CAB15094.1; PID:G2635600
A/Experimental source: strain 168

C:Genetics:
A:Gene: yubA

C:Superfamily: Bacillus subtilis conserved hypothetical protein yueF

Query Match 46.2%; Score 42.5; DB 1; Length 388;

Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 DWNNQMH-DEKN 14
||| | : |||
Db 366 DMFKWQSHYDEKN 380

Search completed: July 29, 2004, 11:37:50
Job time : 10.333 secs

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